```
              GenCore version 5.1.6
       Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:      April 14, 2005, 14:06:59 ; Search time 562 Seconds
                                         (without alignments)
                              10263.124 Million cell updates/sec

Title:        US-10-018-105-3
Perfect score: 3525
Sequence:     1 tatataatatatatatata.........tcaattattcatcaatattgc 3525

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:     1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:     2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  Issued Patents NA:*
   1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
   2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
   3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
   4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
   5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
   6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

	Result No.	Score	% Query Match	Match Length	DB	ID	Description
	1	2155.2	61.1	2358	4	US-09-248-796A-6328	Sequence 6328, Ap
	2	423.8	12.0	507	4	US-09-248-796A-6327	Sequence 6327, Ap
c	3	168.2	4.8	537	3	US-08-998-416-66	Sequence 66, Appl
	4	118.2	3.4	2445	4	US-09-248-796A-6302	Sequence 6302, Ap
	5	73.4	2.1	.708	4	US-09-248-796A-10622	Sequence 10622, A
	6	71.8	2.0	19124	2	US-08-487-826B-13	Sequence 13, Appl
	7	68.8	2.0	1141	4	US-09-806-708B-22	Sequence 22, Appl
	8	68	1.9	767677	4	US-09-949-016-12147	Sequence 12147, A
	9	68	1.9	767677	4	US-09-949-016-17361	Sequence 17361, A
c	10	67.6	1.9	29717	4	US-09-949-016-16284	Sequence 16284, A
c	11	67.6	1.9	60376	4	US-09-949-016-12423	Sequence 12423, A
c	12	66.4	1.9	14066	4	US-09-601-198-56	Sequence 56, Appl
	13	66.4	1.9	19438	4	US-09-949-016-12699	Sequence 12699, A
c	14	66	1.9	26000	4	US-09-843-376-10	Sequence 10, Appl
	15	66	1.9	205044	4	US-09-949-016-15851	Sequence 15851, A
c	16	65.8	1.9	205044	4	US-09-949-016-15852	Sequence 15852, A
c	17	65.8	1.9	205044	4	US-09-949-016-15853	Sequence 15853, A
c	18	65.8	1.9	223471	4	US-09-949-016-12387	Sequence 12387, A
	19	65.8	1.9	223471	4	US-09-949-016-12724	Sequence 12724, A
c	20	65.8	1.9	223471	4	US-09-949-016-12725	Sequence 12725, A
	21	65.2	1.8	1037	4	US-09-181-585-3	Sequence 3, Appli
	22	65.2	1.8	1159	4	US-09-181-585-1	Sequence 1, Appli
	23	65.2	1.8	1471	4	US-09-181-585-2	Sequence 2, Appli
c	24	65	1.8	18773	4	US-09-949-016-14164	Sequence 14164, A
	25	64	1.8	1141	4	US-09-806-708B-22	Sequence 22, Appl
c	26	63.6	1.8	119153	4	US-09-949-016-12378	Sequence 12378, A
c	27	63.4	1.8	837	3	US-08-998-416-288	Sequence 288, App
c	28	63.4	1.8	187169	4	US-09-949-016-12776	Sequence 12776, A
	29	63.4	1.8	191569	4	US-09-949-016-15940	Sequence 15940, A
c	30	62.4	1.8	114139	4	US-09-949-016-16536	Sequence 16536, A
c	31	61.8	1.8	129415	4	US-09-949-016-16997	Sequence 16997, A
c	32	61.8	1.7	147382	4	US-09-949-016-14624	Sequence 14624, A
c	33	61.4	1.7	187169	4	US-09-949-016-12776	Sequence 12776, A
c	34	61.4	1.7	191569	4	US-09-949-016-15940	Sequence 15940, A
	35	61.2	1.7	731	1	US-08-451-405A-2	Sequence 2, Appli
	36	61.2	1.7	3095	6	5231168-1	Patent No. 5231168
	37	61.2	1.7	3095	6	5231168-1	Patent No. 5231168
c	38	61	1.7	1208	4	US-09-949-016-379	Sequence 379, App
c	39	61	1.7	1208	4	US-09-949-016-4309	Sequence 4309, Ap
c	40	61	1.7	194537	4	US-09-949-016-12928	Sequence 12928, A
c	41	61	1.7	201529	4	US-09-949-016-12740	Sequence 12740, A
	42	60.8	1.7	451924	4	US-09-949-016-12896	Sequence 12896, A
	43	60.8	1.7	451925	4	US-09-949-016-17305	Sequence 17305, A
c	44	60.6	1.7	615	3	US-08-998-416-186	Sequence 186, App
	45	60.6	1.7	1039	4	US-09-902-540-1280	Sequence 1280, Ap

ALIGNMENTS

```
RESULT 1
US-09-248-796A-6328
; Sequence 6328, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 6328
;   LENGTH: 2358
;   TYPE: DNA
;   ORGANISM: Candida albicans
US-09-248-796A-6328

Query Match    61.1%;  Score 2155.2;  DB 4;  Length 2358;
Best Local Similarity   97.2%;  Pred. No. 0;
Matches 2293;  Conservative  0;  Mismatches  23;  Indels  44;  Gaps  8;

Qy    285 ATAAATATAATTAAGAGTATATCTCCCCTTTGTTTTTTTTTTCTTCCCAGCCATGTCCG 344
          |||||||||||||||||||||||||||||||| |||||||||||| |||||||||||||
Db      1 ATAAATATAATTAAGAGTATATCTCCCCTTTTG--TTTTTTTCTTCCCAGCCATGTCCG 58

Qy    345 ATAGTGAAAGTTATTATCAAAATTCAACTACTAATCAACCTATTCCTAGATCTGATGAAG 404
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     59 ATAGTGAAAGTTATTATCAAAATTCAACTACTAATCAACCTATTCCTAGATCTGATGAAG 118

Qy    405 TATTGGATGATCATAGAGAATCAAATCACTAATGATTGTGCCATTAGTGATAGTGAAGATG 464
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    119 TATTGGATGATCATAGAGAATCAAATCACTAATGATTGTGCCATTAGTGATAGTGAAGATG 178

Qy    465 AGTTGGAATTAAAATCAGAATTAGAATCAGAAGTTGTAAAAGCGAAA------------ 512
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    179 AGTTGGAATTAAAACCAGAATTAGAATCAGAAGTTGCAAAAAGCGAAAAACAACAACAAC 238

Qy    513 AACAACAACAACATCATCAAGAGATTACATCAGATAATGCTAAACCATTGACTCGTAAAT 572
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    239 AACAACAACAACATCATCAAGAGATTACATCAGATAATGCTAAACCATTGACTCGTAAAT 298

Qy    573 CTGGTTCTTCAATTAAGAAAAAAATCTAATCTTACCGATAAAGATAGAATTACCAACCCTA 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    299 CTGGTTCTTCAATTAAGAAAAAAATCTAATCTTACCGATAAAGATAGAATTACCAACCCTA 358
```

```
Qy   1439 CCCCGATATTCCATCATTAGTATCACCAGGTCAATCTGTTCGAGATTTATTTAGAAATG 1498
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    633 TGAGTTTATCTGGTGGTGTGATGATACTATTAACAGCGGTCACAAAAATCGTAATTATAACA 692

Qy   1752 GTGAAGAAACTTGGTCGTGTTAGAATGTGTTACTTGTCCTACTGATTCGGAAATGAAAATGTTGG 1811
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    359 TGAGTTTATCTGGTGGTGTGATGATACTATTAACAGCGGTCACAAAAATCGTAATTATAACA 418

Qy   1499 GTGAAGAAACTTGGTCGTGTTAGAATGTGTTACTTGTCCTACTGATTCGGAAATGAAAATGTTGG 1558
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    693 TGAGTTTCATTACGTAAAGATTTTATTTAAAAGATAATACTGACGACAATCTACTAATA 752

Qy   1812 CCAAAGCATTGGTATTCATCCTTAACTGCTGAAGATATTCGAAGAACTCGTG 1871
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    419 TGAGTTTCATTACGTAAAGATTTTATTTAAAAGATAATACTGACGACAATCTACTAATA 478

Qy   1559 CCAAAGCATTGGTATTCATCCTTAACTGCTGAAGATATTCGAAGAACTCGTG 1618
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    753 ATCATACTACATCTTGCAATTCCAATTCCAACCCCAATTATTACTAATG 812

Qy   1872 AAAAAGTTGAATTATTAAAAGTTAATTAATTGTTTGTTTTCCATACTTTGAAGCTGATA 1931
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    479 ATCATACTCATCTTGCAATTCCAATTCCAACCCCAATTATTACTAATG 538

Qy   1619 AAAAAGTTGAATTATTAAAAGTTAATTAATTGTTTGTTTTCCATACTTTGAAGCTGATA 1678
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    813 CTAATAAATCAAGAAGAAAATTCAATTGGAAAATTCACCTCCATTAATTAAAAGAGAAAA 872

Qy   1932 AAGAATCTGAACGATTATTAGAACCGATAAAATGTTTATATTGTTGTTTCCATGATGGTA 1991
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    539 CTAATAAATCAAGAAGAAAATTCATTGGAAAATTCACCTCCATTAATTAAAAGAGAAAA 598

Qy   1679 AAGAATCTGAACGATTATTAGAACCGATAAAATGTTTATATTGTTGTTTCCATGATGGTA 1738
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    873 CAATTGGTCGTAAACTAATAATTCTAATAATTTGAAAATGATTTAGTTAGTCCCATGACAAAAA 932

Qy   1992 TATTAACGTTCCATTTTCACCAATTTCTCATCCAGCAAATGTTAGAAGAAGAGTTCGTC 2051
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    599 CTATTGGTCGTAAACTAATAATTCTAATAATTTGAAAATGATTTAGTTAGTCCCATGACAAAAA 658

Qy   1739 TATTAACGTTCCATTTTCACCAATTTCTCATCCAGCAAATGTTAGAAGAAGAGTTCGTC 1798
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    933 TGAAAACTAATAGTGAAGATATTACTAA---TACTAGCACCACTGCTAATCATATGA 989

Qy   2052 AATTGAGAGATTATGTCGATGTTAGTGCTGATTGGTTATGTTATGCCTAATGCATTGAAA 2111
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    659 TGAAAAACTAATAGTGAAGATATTACTACTACTAGCACCACTGCTAATCATATGA 718

Qy   1799 AATTGAGAGATTATGTCGATGTTAGTGCTGATTGGTTATGTTATGCCTAATGCATTGAAA 1858
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    990 AACTTGGTATTGGTGCTACAACCCTTGGTGTTGGAACTGGTACTACCGCCACTGCCACTG 1049

Qy   2112 TTACCGATGGTTTGCCCCCGTGATTCATGGAATTGAATATGAAGCTGATGCCATTGAAG 2171
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    719 AACTTGGTATTGGTGCTACAACCCTTGGTGTTGGAACTGGTACTACCGCCACTGCCACTG 778

Qy   1859 TTACCGATGGTTTGCCCCCGTGATTCATGGAATTGAATATGAAGCTGATGCCATTGAAG 1918
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1050 CCACTGCTGCTGC-------TGGTAGAAGACCATCTCGTTCATCTATTGATAGTGAAG 1100

Qy   2172 ATGCCGTTTCACTGCTGTAGACTACTGATTTTAGTAGTATGTACAAAGAATTGGTGAAT 2231
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    779 CCACTGCTACTGCTGCTGGTGGTGGTGGTAGAAGACCATCTCGTTCATCTATTGATAGTGAAG 838

Qy   1919 ATGCCGTTTCACTGCTGTAGACTACTGATTTTAGTAGTATGTACAAAGAATTGGTGAAT 1978
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1101 CTGATTCTCTCAAGATCATCGCAAGAACTGAAGAGAGATGTTTGTTTTCCTATGG 1160

Qy   2232 CAAGAGAAAAGTCATGACTTAATCGAGATTATTATCAGGTAAAGCTGATGTCATTAAAA 2291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    839 CTGATTCTCTCATGCATCGCAAGAATCATCTCAAGAAACTGAAGAAGAAGATGCTTGTTTTTCCTATGG 898

Qy   1979 CAAGAGAAAAGTCATGACTTAATCGAGATTATTATCAGGTAAAGCTGATGTCATTAAAA 2038
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1161 TTGGTGATCATATTAGAGTTAATGAATTGATTTTGATGAATTAATTGATGAATTTATTAGAG 1220

Qy   2292 TGTTTGCTAAAAGATGTCAAGAAGAGCTAAATTCTTCTTCGGTTATTATCAACGTCAAT 2351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    899 TTGGTGATCATATTAGAGTTAATGAATTGATTTTGATGAATTAATTGATGAATTTATTAGAG 958

Qy   2039 TGTTTGCTAAAAGATGTCAAGAAGAGCTAAATTCTTCTTCGGTTATTATCAACGTCAAT 2098
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1221 AAGAAAAGAGAAGAAGCTTATTTACAAAAACAAATGATTGCTAAAAATATTCTGCGTATTG 1280

Qy   2352 ATAACTTACAACAACAACAACAACA------GGCCCACCACCACCTAATCCTATTA 2405
          ||||||||||||||||||||||||||      ||||||||||||||||||||||||||
Db    959 AAGAAAAGAGAAGAAGCTTATTTACAAAAACAAATGATTGCTAAAAATATTCTGCGTATTG 1018

Qy   2099 ATAACTTACAACAACAACAACGACAACAACAGGGCCCACCACCACCTAACCCTATTA 2158
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1281 ATGAAATTTCAAAATCTTCAAAAATAATACTACTAGTGCGCATCTCGTCATCCATATC 1340

Qy   2406 TTACTTCACCAATTAATTCAACTTTGAATCTTTAATAGTTTAGGAACTTCAACTGGTGGAG 2465
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1019 ATGAAATTTCAAAATCTTCAAAAATAATACTACTAGTGCGCATCTCGTCATCCATATC 1078

Qy   2159 TTACTTCACCAATTAATTCAACTTTGAATCTTTAATAGTTTAGGAACTTCAACTGGTGGAG 2218
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1341 ATCATCACAGTAATAATAATAAAAAAAAATAATAATGGTGGTGATG---GTGGTGGTTCTAGTA 1397

Qy   2466 GAGTAGGAGTAGGACGACGGAATTAATTTTGGTCCCAATCTGGAAATAATATAATACTA 2525
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1079 ATCATCACAGTAATAATAATAATAATAAAAAAAAATAATGGTGATGGTGGTAGTGGTTCTAGTA 1138

Qy   2219 GAGTACGAGTACGACGACGGAATTAATTTTGGTCCCCATCCAACCTGGAAATAATACTAATACTA 2278
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1398 TGGCAGCATTAAAAATATACTTCAAAAAATATTTAAAGAAACATTATCAAGATTTGAAT 1457

Qy   2526 ATACTAATACTACTGGTTCACCTGTTCACCTTCACCTACCACCT---CAACTACAAACACATGTATCACTA 2585
          ||||||||||||||||||||||||||||||||||||||||||||      |||||||||||||||||||||
Db   1139 TGGCAGCATTAAAAATATACTTCCAAAAATATTTAAAGAAACATTATCAAGATTTGAAT 1198

Qy   2279 ATACTAACACTACGGGGTTCACCTTGACCTTCACCTACCACCT---CAACTACAAACACATGTATCACTA 2335
          ||||||||||||||||||||||||||||||||||||||||||||      |||||||||||||||||||||
Db   1458 TTACTTCATGAAAATCTTCATCTCTTCAGAAGAAATTTATGAATTGAAGACTAAACAAC 1517

Qy   2586 ACAAATCTTTCCCCATCCCC 2605
          ||||||||||||||||||||
Db   1199 TTACTTCATGAAAATCTTCATCTCTTCAGAAGAAATTTATGAATTGAAGACTAAACAAC 1258

Qy   2336 ACAAATCTTTCCCCATCCCC 2355
          ||||||||||||||||||||
Db   1518 CACCTTACAAAATCTCTGGGATCCTGGGCAGTGAAATTTCGTGGAGCAAGAATTTTCTGATGGGATTAATG-----T 1571

Db   1259 CACCTTACAAATACAAATGATGATCAAAATATGATCAAATTTCAATCAAATTAACTTCATCATCCACTT 1318

Db   1572 CTGGATCTCGGATCTCGGGCAGTGAAATTTCGTGGAGCAAGAATTTTCTGATGGGATTAATG 1631

Db   1319 CTGGATCTCGGATCTCGGGCAGTGAAATTTCGTGGAGCAAGAATTTTCTGATGGGATTAATG 1378

Db   1632 GAGGTTCATTACCTGATAGATTTTCACTTTTCCATTTCTGAATCAGAAGAAACTATTCATG 1691

Db   1379 GAGGTTCATTACCTGATAGATTTTCACTTTTCCATTTCTGAATCTGAATCAGAAGAAACTATTCATG 1438

Db   1692 CCCCGATATTCCATCATTAGTATCACCAGGTCAATCTGTTCGAGATTTATTTAGAAATG 1751
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 13:36:05 ; Search time 1739 Seconds
                                         (without alignments)
                              11999.476 Million cell updates/sec

Title: US-10-018-105-3
Perfect score: 3525
Sequence: 1 tatatatatatataata.........tcaattattatcaatattgc 3525

Scoring table: IDENTITY NUC .
                Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 295987O667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :   N_Geneseq_16Dec04:*
         1: geneseqn1980s:*
         2: geneseqn1990s:*
         3: geneseqn2000s:*
         4: geneseqn2001as:*
         5: geneseqn2001bs:*
         6: geneseqn2002as:*
         7: geneseqn2002bs:*
         8: geneseqn2003as:*
         9: geneseqn2003bs:*
        10: geneseqn2003cs:*
        11: geneseqn2003ds:*
        12: geneseqn2004as:*
        13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Pred. No.	Description
1	3523	99.9	3525	3	AAC87954		Aac87954 Candida a
2	2769	78.6	2769	6	ABZ32388		Abz32388 Candida a
3	263.8	7.5	684	8	ABN21722		Abn21722 Human ORF
4	179.6	5.1	1992	8	ABT19393		Abt19393 Aspergill
5	179.6	5.1	1992	8	ABT21213		Abt21213 Aspergill
6	169.4	4.8	860	2	ABZ51492		Abz51492 Aspergill
7	168.2	4.8	537	2	ADR01374		Adr01374 A. gossyp
8	118	3.3	462	6	ABN76186		Abn76186 Human gly
9	117.6	3.3	8056	8	ABZ10246		Abz10246 Haematopo
10	116.4	3.3	688	3	AAF14580		Aaf14580 Aspergill
11	113.6	3.2	2048	8	ABT20615		Abt20615 Aspergill
12	113.6	3.2	2048	8	ABT18799		Abt18799 Aspergill
13	113.6	3.2	4048	8	ABT18205		Abt18205 Aspergill
14	113.6	3.2	4048	8	ABT20019		Abt20019 Aspergill
15	113.6	3.2	7990	13	ADR84473		Adr84473 Aspergill
16	107.8	3.1	321	6	ABN22505		Abn22505 Human ORF
17	106.8	3.0	4985	6	ABQ75107	c	Abq75107 Anopheles
18	106.8	3.0	4985	10	ACF79720	c	Acf79720 Mosquito
19	106.2	3.0	575	3	AAF07924		Aaf07924 Fusarium
20	94.4	2.7	969	6	ABQ39490	c	Abq39490 Oligonucl

21	94.4	2.7	969	6	ABQ39491	Abq39491 Oligonucl
22	92.6	2.6	8056	8	ABZ10246	Abz10246 Haematopo
23	c	90	2.6	3996	6	AAD47004	Aad47004 Plasmodiu
24	86.6	2.5	8056	8	ABZ10100	Abz10100 Haematopo
25	85.8	2.4	2000	10	ADK62467	Adk62467 Disease t
26	c	84.8	2.4	8056	8	ABZ10100	Abz10100 Haematopo
27	84	2.4	7676	6	ABL34598	Abl34598 Human met
28	84	2.4	7676	6	ABL70409	Abl70409 Chemical1
29	84	2.4	7676	7	ADS99859	Ads99859 Bisulphit
30	81.2	2.3	4985	6	ABQ75107	Abq75107 Anopheles
31	81.2	2.3	4985	10	ACF79720	Acf79720 Mosquito
32	79.8	2.3	6033	3	AAA70152	Aaa70152 Plasmodiu
33	79.8	2.3	9859	13	ADS89440	Ads89440 Oligonucl
34	79.8	2.3	9859	13	ADS89714	Ads89714 Oligonucl
35	79.6	2.3	3931	9	ACC84661	Acc84661 P. falcip
36	c	78.2	2.2	8759	8	ABZ10238	Abz10238 Haematopo
37	c	78.2	2.2	8759	8	ABZ09964	Abz09964 Haematopo
38	c	78.2	2.2	8759	8	ABZ10092	Abz10092 Haematopo
39	c	78.2	2.2	8759	8	ABZ10110	Abz10110 Haematopo
40	c	78.2	2.2	8759	10	ADB54086	Adb54086 Pretreate
41	c	78.2	2.2	8759	10	ADB54214	Adb54214 Pretreate
42	c	78.2	2.2	8759	10	ADE84072	Ade84072 Human lym
43	c	78.2	2.2	8759	10	ADE84148	Ade84148 Human lym
44	c	78.2	2.2	8759	13	ADS89514	Ads89514 Oligonucl
45	c	78.2	2.2	8759	13	ADS89240	Ads89240 Oligonucl

ALIGNMENTS

RESULT 1
AAC87954
ID   AAC87954 standard; DNA; 3525 BP.
XX
AC   AAC87954;
XX
DT   06-MAR-2001 (first entry)
XX
DE   Candida albicans CaALR1 nucleotide sequence.
XX
KW   Candida albicans; yeast pathogen; identification; fungal; antifungal;
KW   CaKRE5; CaALR1; CaCDC24; diagnosis; fungicide; fungal infection; ds.
XX
OS   Candida albicans.
XX
PN   WO200068420-A2.
XX
PD   16-NOV-2000.
XX
PF   05-MAY-2000; 2000WO-CA000533.
XX
PR   05-MAY-1999; 99US-0132878P.
XX
PA   (MYCO-) MYCOTA BIOSCIENCES INC.
XX
PI   Roemer T, Bussey H, Davison J;
XX
DR   WPI; 2000-687652/67.
DR   P-PSDB; AAB36515.
XX
PT   New DNA encoding essential proteins of Candida albicans, useful for
PT   diagnosing fungal infections and to screen for clinical or agricultural
PT   antifungal agents.
XX
PS   Claim 3; Fig 2A; 76pp; English.
XX
CC   The present sequence represents the fungus-specific Candida albicans gene
CC   CaALR1. The present invention describes the fungus-specific genes CaKRE5,
CC   CaALR1 and CaCDC24 isolated in the yeast pathogen C. albicans. The genes
CC   have antifungal and fungicide activity. The genes in C. albicans and are
CC   useful as drug targets. Fragments of them are useful as probes and
CC   primers for diagnosis of fungal infections, also as antisense and
CC   ribozyme agents. Proteins encoded by the genes are used to screen for

```
CC   their specific inhibitors which are potential antifungal agents for
CC   controlling a wide range of fungi pathogenic on animals or plants.
CC   Fragments of the proteins are also used to raise specific antibodies.
CC   Higher animals do not contain genes closely similar to the C. albicans
CC   genes, so antifungal agents that target them are less likely to be toxic
XX   to humans
SQ   Sequence 3525 BP; 1256 A; 525 C; 546 G; 1196 T; 0 U; 2 Other;

Query Match     99.9%;  Score 3523;  DB 3;  Length 3525;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 3525;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
```

```
Qy       1 TATATATATATATATAAACATAAACAACTAAATAAAAAAAAACTTCATATTTTCAACTGTT 60
           ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TATATAATATATATATAAACATAAACAACTAAATAAAAAAAAACTTCATATTTTCAACTGTT 60

Qy      61 CAACCCAACACCCCCCGTGTCCTAGTCTCAGTCCTCAGTCCTTAGTTCTAATATTGTTGATT 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CAACCCAACACCCCCCGTGTCCTAGTCTCAGTCCTCAGTCCTTAGTTCTAATATTGTTGATT 120

Qy     121 AATTAAACAGTCACTAGTCCTCAGTCCTCAGTCTTAGTCTTGGTTCTTAATATTAAGA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AATTAAACAGTCACTAGTCCTCAGTCCTCAGTCTTAGTCTTGGTTCTTAATATTAAGA 180

Qy     181 TNTTCCATTTTTTTTTTTTTTTACCCAAGCTATGAAAAATTATTTTGTTGTCTAACAACTATA 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TNTTCCATTTTTTTTTTTTTTTACCCAAGCTATGAAAAATTATTTTGTTGTCTAACAACTATA 240

Qy     241 ATAATATTTACCAGAAATTGCTACAAATAAATAAATAAATAAAATATAATTAAGA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ATAATATTTACCAGAAATTGCTACAAATAAATAAATAAATAAAATATAATTAAGA 300

Qy     301 GTATATCTCCCCTTTGTTTTTTTTGTTTTTTTTTCTTCCCAGCCATGTCCGATAGTGAAGTTATTA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GTATATCTCCCCTTTGTTTTTTTTGTTTTTTTTTCTTCCCAGCCATGTCCGATAGTGAAGTTATTA 360

Qy     361 TCAAAAATTCAACTACTAATCAACCTATTCCTAGATCTGATCTGAGTATTGGATGATCATAG 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TCAAAAATTCAACTACTAATCAACCTATTCCTAGATCTGATCTGAGTATTGGATGATCATAG 420

Qy     421 AAATCAAATCACTAATGATTGTGCCATTAGTGATAGTGAAGATGAGTTGGAATTAAAAATC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AAATCAAATCACTAATGATTGTGCCATTAGTGATAGTGAAGATGAGTTGGAATTAAAAATC 480

Qy     481 AGAATTAGAATCAGAAGTTGTAAAAGCGAAAAACAACAACAACATCATCAAGAGATTAC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AGAATTAGAATCAGAAGTTGTAAAAGCGAAAAACAACAACAACATCATCAAGAGATTAC 540

Qy     541 ATCAGATAATGCTAAACCATTGACTCGTAAATCTGGTTCTTCAATTAAGAAAAATCTAA 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 ATCAGATAATGCTAAACCATTGACTCGTAAATCTGGTTCTTCAATTAAGAAAAATCTAA 600

Qy     601 TCTTACCGATAAAGATAGAATTACCAACCCTATGAGTTATCTGGTGGTGATGATACTAT 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TCTTACCGATAAAGATAGAATTACCAACCCTATGAGTTATCTGGTGGTGATGATACTAT 660

Qy     661 TAACAGCGGTCACAAAATCGTAATTATAACATGAGTTCATTACGTAAAGATTTTTATTT 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TAACAGCGGTCACAAAATCGTAATTATAACATGAGTTCATTACGTAAAGATTTTTATTT 720

Qy     721 AAAAGATAATACTGACGACAATTCACTACTAATAATCATCATCTGAAGTTCCAATTCC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AAAAGATAATACTGACGACAATTCACTACTAATAATCATCATCTGAAGTTCCAATTCC 780

Qy     781 AATTCCAATTCCAACCCAATTATTACTAATGCTAATAAATCAAGAAGAAAATCTCAATT 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AATTCCAATTCCAACCCAATTATTACTAATGCTAATAAATCAAGAAGAAAATCTCAATT 840

Qy     841 GGAAAATTTACCTCCATTAATTAAAAAGAAAACAATTGGTCGTAATAATTCTAATAATTT 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 GGAAAATTTACCTCCATTAATTAAAAAGAAAACAATTGGTCGTAATAATTCTAATAATTT 900
```

```
Qy     901 TGAAAATGATTTAGTTAGTTAGTCCCATGACAAAAATGAAAAACTAATGATAGTGAAGATATTAC 960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 TGAAAATGATTTAGTTAGTTAGTCCCATGACAACAAAAATGAAAAACTAATGATAGTGAAGATATTAC 960

Qy     961 TAATACTAGCACCACTGCTAATCATCATATGAAACTTGGTATTGGTGCTACAACCCTTGGTGT 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TAATACTAGCACCACTGCTAATCATCATATGAAACTTGGTATTGGTGCTACAACCCTTGGTGT 1020

Qy    1021 TGGAACTGTACTACCGCCACTGCCACTGCCACTGCCACTGCGTGGTGTAGAGACCATCTCG 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TGGAACTGTACTACCGCCACTGCCACTGCCACTGCCACTGCGTGGTGTAGAGAACCATCTCG 1080

Qy    1081 TTCATCTATTGATAGTGAAGCTGATTCTCATGACATCAAGATCATCTCAAGAAACTGAAGA 1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 TTCATCTATTGATAGTGAAGCTGATTCTCATGACATCAAGATCATCTCAAGAAACTGAAGA 1140

Qy    1141 AGATGTTTGTTTTCCTATGGTTGTGATCATATTAGAGTAATTGATTTTGATGA 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 AGATGTTTGTTTTCCTATGGTTGTGATCATATTAGAGTAATTGATTTTGATGA 1200

Qy    1201 AATTGATGAATTATTAGAGAAGAAGAAGAAGAGAAAGAAGAGCTTATTTACAAAAACAAATGATTGC 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 AATTGATGAATTATTAGAGAAGAAGAAGAAGAGAAAGAAGAGCTTATTTACAAAAACAAATGATTGC 1260

Qy    1261 TAAAAATATTCTGCGTATTGATGAATTCAAAATCTTTCCAAAATCTTTCCAAAAATAATACTACTAGTCG 1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TAAAAATATTCTGCGTATTGATGAATTCAAAATCTTTCCAAAATCTTTCCAAAAATAATACTACTAGTGG 1320

Qy    1321 TGCATCTCGTCATCCATATCATCCACAGTAATAATAATAAAAAAAATAATGGTGGTGA 1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 TGCATCTCGTCATCCATATCATCCACAGTAATAATAATAAAAAAAATAATGGTGGTGA 1380

Qy    1381 TGGTGGTGGTTCCTTAGTATGGCAGCCATGTCGGATCTGGGCAGGTGAAATTTGGGACGAAGAATTTCTGA 1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 TGGTGGTGGTTCCTTAGTATGGCAGCCATGTCGGATCTGGGCAGGTGAAATTTGGGACGAAGAATTTCTGA 1440

Qy    1441 ATTATCAAGATTTGAATTTACTCATGAAGAAATTCTTCATCTTCAGAAGAAATTTATGAATT 1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 ATTATCAAGATTTGAATTTACTCATGAAGAAATTCTTCATCTTCAGAAGAAATTTATGAATT 1500

Qy    1501 GAAGACTAAACAACAACACCACCTTACAAATATGATCAAATATCATTCATCTCATCTAC 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 GAAGACTAAACAACAACACCACCTTACAAATATGATCAAATATCATTCATCTCATCTAC 1560

Qy    1561 ATCTTCACTTCTGGATCTGGATCTGGGCAGGTGAAATTTGGTGGAGCAAGAATTTCTGA 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 ATCTTCACTTCTGGATCTGGATCTGGGCAGGTGAAATTTGGTGGAGCAAGAATTTCTGA 1620

Qy    1621 TGGGATTAATGGAGGTTCATTACCTGATAGATTTCCATTCGAAGATTCGAATCAGAGA 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 TGGGATTAATGGAGGTTCATTACCTGATAGATTTCCATTCGAAGATTCGAATCAGAGA 1680

Qy    1681 AACTATTCATGCCCCCGATATTCCATCATTAGTATCACCAGTCAATCTGTTCGAGATTT 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 AACTATTCATGCCCCCGATATTCCATCATTAGTATCACCAGTCAATCTGTTCGAGATTT 1740

Qy    1741 ATTTAGAAATGTGGCCAAAGCATTTGGTATTCATCCTTAACTGCTGAAGATATTCGAATGCA 1800
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 ATTTAGAAATGTGGCCAAAGCATTTGGTATTCATCCTTAACTGCTGAAGATATTCGAATGCA 1800

Qy    1801 GAAAATGTTGGCCAAAGCATTTGGTATTCATCCTTAACTGCTGAAGATATTCGAATGCA 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 GAAAATGTTGGCCAAAGCATTTGGTATTCATCCTTAACTGCTGAAGATATTCGAATGCA 1860

Qy    1861 AGAAACTCGTGAAAAAGTTGAATTATTAAAGTTATATTTTGTTTTGTTCCATACTTT 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 AGAAACTCGTGAAAAAGTTGAATTATTAAAGTTATATTTTGTTTTGTTCCATACTTT 1920

Qy    1921 TGAAGCTGATAAAGATCTGAAGATTATTTAGAACCGATAAAGTTTATATTGTTGTTTT 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 TGAAGCTGATAAAGATCTGAAGATTATTTAGAACCGATAAAGTTTATATTGTTGTTTT 1980

Qy    1981 CCATGATGGTATATTAACGTTCCATTTTTCACCAATTTCTCATCCAGCAAATGTTAGAAG 2040
```

```
Db   1981 CCATGATGCTATATTAACGTTCCATTTTCCACCAATTTTCTCATCCAGCAAATGTTAGAAG 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   2041 AAGAGTTCGTCAATTGAGAGATTATGTCGATGTTAGTGCTGATGGTTATGTTATGCCCTT 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AAGAGTTCGTCAATTGAGAGATTATGTCGATGTTAGTGCTGATGGTTATGTTATGCCCTT 2100

Qy   2101 AATCGATGAAATTACCGATGGTTTGCCCCCGTGATTCATGGAATTGAATATGAAGCTGA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 AATCGATGAAATTACCGATGGTTTGCCCCCGTGATTCATGGAATTGAATATGAAGCTGA 2160

Qy   2161 TGCCATTGAAGATGCCGTTTCACTGCTAGAGATACTGATTTTAGTAGTAGTGTTACAAAG 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 TGCCATTGAAGATGCCGTTTCACTGCTAGAGATACTGATTTTAGTAGTAGTGTTACAAAG 2220

Qy   2221 AATTGGTGAATCAAGAAGAAAGTCATGACTTTAATGAGATTATTATCAGGTAAAGCTGA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 AATTGGTGAATCAAGAAGAAAGTCATGACTTTAATGAGATTATTATCAGGTAAAGCTGA 2280

Qy   2281 TGTCATTAAAAATGTTGCTAAAAGATGTCAAGAAGAGAAGTAATTCTTCTTCTCGGTTATTA 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TGTCATTAAAAATGTTGCTAAAAGATGTCAAGAAGAGAAGTAATTCTTCTTCTCGGTTATTA 2340

Qy   2341 TCAACGTCAATATAACTTACAACACAACAACAACAGGCCCCCACCACCTAATCC 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TCAACGTCAATATAACTTACAACACAACAACAACAGGCCCCCACCACCTAATCC 2400

Qy   2401 TATTAATTACTTCACCAATTAATCAACTTGAATCTTAATAGTTTAGGAACTTCAACTGG 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TATTAATTACTTCACCAATTAATCAACTTGAATCTTAATAGTTTAGGAACTTCAACTGG 2460

Qy   2461 TGGAGGAGTAGGAGGTAGGAGGAATTAATTTGGTCCCAATCCAACTGGAAATAATACTAA 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 TGGAGGAGTAGGAGGTAGGAGGAATTAATTTGGTCCCAATCCAACTGGAAATAATACTAA 2520

Qy   2521 TACTAATACTAATACTACTGGTTCACCTTCACCACCTCAACACAACAACAACAACATGGTAT 2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 TACTAATACTAATACTACTGGTTCACCTTCACCACCTCAACACAACAACAACAACATGGTAT 2580

Qy   2581 CACTAACAAATCTTCCCCATCCCGATGCACGTCCAAGAGCTCGATATTGCATTATATATT 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 CACTAACAAATCTTCCCCATCCCGATGCACGTCCAAGAGCTCGATATTGCATTATATATT 2640

Qy   2641 AGGTGATATTCAAGATCATATATCACCATGTTTCAAAATTTATTAGCCTATGAAAAAAT 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 AGGTGATATTCAAGATCATATATCACCATGTTTCAAAATTTATTAGCCTATGAAAAAAT 2700

Qy   2701 TTTCAGTGTTCACATTCAAATTATTAGCTCAATTACAAGTTGAATCATTCAATTCCAA 2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 TTTCAGTGTTCACATTCAAATTATTAGCTCAATTACAAGTTGAATCATTCAATTCCAA 2760

Qy   2761 TAATAAAATCACCGAAATGTTTCTAAATTACTTGATTGGGACAATGTTAGTTCCATT 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TAATAAAATCACCGAAATGTTTCTAAATTACTTGATTGGGACAATGTTAGTTCCATT 2820

Qy   2821 AAATTTAGTCACGGGACTTTTGTGTATGAAGTGAAGGTGTACCAA 2880
          |||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AAATTTAGTCACGGGACTTTTGTGTATGAAGTGAAGGTGTACCAA 2880

Qy   2881 TTTAGGTTGGTTTTTCGGAATTGTTGGTAGTATTAATTATATATTTTATAATTTGGATCATTTAT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 TTTAGGTTGGTTTTTCGGAATTGTTGGTAGTATTAATTATATATTTTATAATTTGGATCATTTAT 2940

Qy   2941 ATTTGCTCAATGTGGTTGAAAAATTGAATAAATTCAATTGAAGGACAAAATAATGGTAA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 ATTTGCTCAATGTGGTTGAAAAATTGAATAAATTCAATTGAAGGACAAAATAATGGTAA 3000

Qy   3001 TCGACCAATTTTAATCATCAAGAAGATCAATTAGAAGTTTAGGTTTAAAAAACA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 TCGACCAATTTTAATCATCAAGAAGATCAATTAGAAGTTTAGGTTTAAAAAACA 3060

Qy   3061 TGGTGGTAATAAATCAATTATTAGTTTCCCAATAAATGATAAGAATAATCAAAGAA 3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 TGGTGGTAATAAATCAATTATTAGTTCCCAATAAATGATAAGAATAATCAAAGAA 3120

Qy   3121 ATGCCACAGAGTTGATGGTTGTTGTTTTTTTTTTTTTTATTGTCATGATGGAGTTGTATAT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 ATGCCACAGAGTTGATGGTTGTTGTTTTTTTTTTTTTTATTGTCATGATGGAGTTGTATAT 3180

Qy   3181 ACATATACTTTTATAGAGTAACAATAGTAAATGATAATGATAATAGTCATCAATCATCATA 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 ACATATACTTTTATAGAGTAACAATAGTAAATGATAATGATAATAGTCATCAATCATCATA 3240

Qy   3241 TTTAATTGTATATAATCGTATACTAACTCTTCTCTTGATTTAGGGAAAGAGTTATATTA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TTTAATTGTATATAATCGTATACTAACTCTTCTCTTGATTTAGGGAAAGAGTTATATTA 3300

Qy   3301 TTTACTATAAACATTTATTTTTACGAGTTGTGTTAAATTGGAGAGTCAAATTAATAGGAT 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 TTTACTATAAACATTTATTTTTACGAGTTGTGTTAAATTGGAGAGTCAAATTAATAGGAT 3360

Qy   3361 GTAAAGAGAGTTTTTAAAGAAGGAATAAAGAAATATTATAATTCAGANGTTCATACAGAA 3420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GTAAAGAGAGTTTTTAAAGAAGGAATAAAGAAATATTATAATTCAGANGTTCATACAGAA 3420

Qy   3421 GGGGGGGGAAGGAGGAAGGGGATATATATCGGCATTGTTGGTACTTTTGTTTTTGAAATA 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 GGGGGGGGAAGGAGGAAGGGGATATATATCGGCATTGTTGGTACTTTTGTTTTTGAAATA 3480

Qy   3481 AAATATAAGTTATCTAAATTATTATCAATTATTATCAATATTGC 3525
          |||||||||||||||||||||||||||||||||||||||||||
Db   3481 AAATATAAGTTTATCTAAATTATTATCTAAATTATTATCAATTATTATCAATATTGC 3525
```

RESULT 2
AB232388

```
ID   AB232388  standard; DNA; 2769 BP.
XX
AC   AB232388;
XX
DT   30-JAN-2003  (first entry)
XX
DE   Candida albicans essential gene SEQ ID NO 6675.
XX
KW   Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
KW   signal transduction; DNA replication; cell division; growth;
KW   proliferation; Candida albicans; fungicide; antifungal; gene; ss.
XX
OS   Candida albicans.
XX
PN   WO200253728-A2.
XX
PD   11-JUL-2002.
XX
PF   26-DEC-2001; 2001WO-US049486.
XX
PR   29-DEC-2000; 2000US-0259128P.
PR   20-FEB-2001; 2001US-00792024.
PR   22-AUG-2001; 2001US-0314050P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
XX
DR   WPI; 2002-566694/60.
DR   P-PSDB; ABP73838.
XX
PT   Constructing strains for identifying gene products as effective targets
PT   for therapeutic intervention, by inactivating in the strain one allele of
PT   a gene and placing other allele of the gene under conditional expression.
XX
PS   Claim 37; SEQ ID NO 6675; 167pp + Sequence Listing; English.
XX
CC   The invention relates to constructing (M1) a strain of diploid fungal
CC   cells in which both alleles of a gene are modified, comprising modifying
CC   one allele by insertion or replacement by a cassette having an
```

```
                 GenCore version 5.1.6
        Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:   April 14, 2005, 13:38:30 ; Search time 14937 Seconds
                                     (without alignments)
                          11435.003 Million cell updates/sec

Title:            US-10-018-105-3
Perfect score:    3525
Sequence:         1 tatatacatatatatata........tcaattattatcaatattgc 3525

Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched:         4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters:      9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :  GenEmbl:*
     1: gb_ba:*
     2: gb_htg:*
     3: gb_in:*
     4: gb_om:*
     5: gb_ov:*
     6: gb_pat:*
     7: gb_ph:*
     8: gb_pl:*
     9: gb_pr:*
    10: gb_ro:*
    11: gb_sts:*
    12: gb_sy:*
    13: gb_un:*
    14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution:
```

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		3523	99.9	3525	6	BD273775	BD273775 Identific
2		3523	99.9	3525	6	AX046919	AX046919 Sequence
3		2769	78.6	2769	6	AX489375	AX489375 Sequence
4		2155.2	61.1	2358	6	AR551197	AR551197 Sequence
c 5		581	16.5	110000	8	CR382138_14	Continuation (15 o
6		423.8	12.0	507	6	AR551196	AR551196 Sequence
7		396	11.2	2580	8	AY692762	AY692762 Saccharom
8		396	11.2	4202	8	SCYOL130W	U74872 S.cerevisia
9		396	11.2	13421	8	SCU41293	U41293 Saccharomyc
10		385	10.9	110000	8	CR380951_1	CR380951 Continuation (2 of
11		383	10.7	270148	8	YSCCHRVIN	YSCCHRVIN Continuation (7 of
c 12		376	10.7	110000	8	CR382125_06	Continuation (7 of
c 13		373.6	10.6	110000	8	AE016817_03	Continuation (4 of
14		263.8	7.5	684	8	CQ446161	CQ446161 Sequence
c 15		252.4	7.2	35030	8	SPBC27B12	S.pombe c
16		252.4	7.2	38000	8	AB004539	AB004539 Schizosac
17		252.4	7.2	38911	8	AB004538	AB004538 Schizosac
18		215	6.1	110000	8	CR382130_00	CR382130 Yarrowia
19		191.2	5.4	43880	8	SPAC17G6	Z99162 S.pombe chr
20		190.8	5.4	110000	8	CR382131_00	CR382131 Yarrowia
21		176.8	5.0	875	11	CNS06F3M	AL395912 T7 end of
22	c	172.4	4.9	163843	5	BX510939	BX510939 Zebrafish
23	c	172.4	4.9	211113	2	CR391962	CR391962 Danio rer
24	c	169.8	4.8	110000	6	CR380959_12	Continuation (13 o
25	c	168.2	4.8	537	6	A85407	A85407 Sequence 66
26	c	168.2	4.8	537	6	AR154900	AR154900 Sequence
27	c	168.2	4.8	537	6	B65425	B65425 Genome DNA
28	c	150.6	4.3	110000	8	CR382137_08	Continuation (9 of
29		149	4.2	94534	5	AL929250	AL929250 Zebrafish
30		145.4	4.2	173019	5	BX321884	BX321884 Zebrafish
31	c	145	4.1	238084	2	BX950172	BX950172 Danio rer
32		144	4.1	34347	2	BX957360	BX957360 Danio rer
33	c	142.8	4.1	155204	2	AC007926	AC007926 Trypanoso
34		142	4.0	177575	5	AL953867	AL953867 Zebrafish
35	c	141.8	4.0	143342	2	CR388191	CR388191 Danio rer
36	c	140.2	4.0	145306	2	BX899179	BX899179 Danio rer
37		140.2	4.0	145553	5	AL935272	AL935272 Zebrafish
38		138.2	3.9	154071	3	AC115598	AC115598 Dictyoste
39		130.2	3.7	115990	5	BX890614	BX890614 Zebrafish
40	c	127.6	3.6	203127	5	BX322566	BX322566 Zebrafish
41		127.4	3.6	3957	8	SCYKL064W	Z28064 S.cerevisia
42		127.4	3.6	28600	8	SCK1286K	X75781 S.cerevisia
43	c	126.8	3.6	100893	8	CR380959_13	Continuation (14 o
44	c	126.2	3.6	146415	5	AL929469	AL929469 Zebrafish
45		126.2	3.6	170800	2	CR352223	CR352223 Danio rer

ALIGNMENTS

```
RESULT 1
BD273775

LOCUS       BD273775                3525 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Identification of candida albicans essential fungal specific genes
            and use thereof in antifungal drug discovery.
ACCESSION   BD273775
VERSION     BD273775.1  GI:33083543
KEYWORDS    JP 200254799-A/2.
SOURCE      Candida albicans
ORGANISM    Candida albicans
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE   1  (bases 1 to 3525)
AUTHORS     Roemer,T., Bussey,H. and Davison,J.
TITLE       Identification of candida albicans essential fungal specific genes
            and use thereof in antifungal drug discovery
JOURNAL     Patent: JP 200254799-A 2 24-DEC-2002;
            MCGILL UNIVERSITY
COMMENT     OS  Candida albicans
            PN  JP 200254799-A/2
            PD  24-DEC-2002
            PF  05-MAY-2000 JP 2000616385
            PR  05-MAY-1999 US 60/132878
            PI  TERRY ROEMER,HOWARD BUSSEY,JOHN DAVISON
            PC  C12N15/09,C07K14/40,C07K16/14,C12Q1/68,G01N33/50, PC
            G01N33/569,
            PC  C12N15/00
            CC  Identification of candida albicans essential fungal specific
            CC      genes and use
            CC  thereof in antifungal drug discovery
            FH  Key             Location/Qualifiers
            FT  CDS             (338)..(3103).
FEATURES             Location/Qualifiers
     source          1..3525
                     /organism="Candida albicans"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:5476"
ORIGIN

Query Match             99.9%;  Score 3523;  DB 6;  Length 3525;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy      1 TATATATATATATATAAACATAACATATTAAAAAAACTTCATATTTAAAAAAACTTCAACTGTT   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TATATAATAATAATAATAAACATAACATATTAAAAAAAACTTCATATTTGTTCAACTGTT      60

Qy     61 CAACCCACACCCCGTGTTCCTAGTCTCAGTTCCAATTTATTAAGTCATATATTGTTCATT    120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CAACCCACACCCCGTGTTCCTAGTCTCAGTTCCAATTTATTAAGTCATATATTGTTGATT    120

Qy    121 AATTAAACAGTCACTAGTCCTCAGTCCTCCTAGTTCTTGGTTCTTAATATTATTAAGA    180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AATTAAACAGTCACTAGTCCTCAGTCCTCCTAGTTCTTGGTTCTTAATATTAATTAAGA    180

Qy    181 TNTTCCATTTTTTTTTTTTTACCCAAGCTATGAAAATTATTTTTGTTGTCTAACAACTATA    240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TNTTCCATTTTTTTTTTTTTACCCAAGCTATGAAAATTATTTTTGTTGTCTAACAACTATA    240

Qy    241 ATAATATTTACCAGAAATTGCTACAAATATAAATAAATAAAATAAATAATTAAGA    300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATAATATTTACCAGAAATTGCTACAAATATAAATAAATAAAATAAATAATTAAGA    300

Qy    301 GTATATCTCCCCCTTTGTTTTTTTTTCTTCCCAGCCATGTCCGATAGTGAAAGTTATTA    360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTATATCTCCCCCTTTGTTTTTTTTTCTTCCCAGCCATGTCCGATAGTGAAAGTTATTA    360

Qy    361 TCAAAATTCAACTACTAATCAACCATTCCTAGATCGTAAGTTCTTCAATTGGATGATCATAG    420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TCAAAATTCAACTACTAATCAACCATTCCTAGATCGTAAGTATTGGATGATGATCATAG    420

Qy    421 AAATCAAATCACTAATGATTGTGCCATTAGTGATGATGAGTTGGAATTAAAATC    480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AAATCAAATCACTAATGATTGTGCCATTAGTGATGATGAGTTGGAATTAAAATC    480

Qy    481 AGAATTAGAATCAGAAGTTGTAAAAAGCGAAAACAACAACAACAACATCATCAAGAGATTAC    540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AGAATTAGAATCAGAAGTTGTAAAAAGCGAAAACAACAACAACAACATCATCAAGAGATTAC    540

Qy    541 ATCAGATAATGCTAAACCATTGACTCGTAAATCTGGTTCTTCAATTAAGAAAAAATCTAA    600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ATCAGATAATGCTAAACCATTGACTCGTAAATCTGGTTCTTCAATTAAGAAAAAATCTAA    600

Qy    601 TCTTACCGGATAAAGATAGAATTACCAACCCTATGAGTTTATCTGGTGGTGATGATACTAT    660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TCTTACCGGATAAAGATAGAATTACCAACCCTATGAGTTTATCTGGTGGTGATGATACTAT    660

Qy    661 TAACAGCGGTCACAAAAATCGTAATTATAAACATGAGTTCATTACGTAAAGATTTTTATT    720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TAACAGCGGTCACAAAAATCGTAATTATAAACATGAGTTCATTACGTAAAGATTTTTATT    720

Qy    721 AAAAGATAATACTGACGACAATTCTACTAATAATCATCACTAATCATCTTGCAATTCCAATTCC    780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AAAAGATAATACTGACGACAATTCTACTAATAATCATCACTAATCATCTTGCAATTCCAATTCC    780

Qy    781 AATTCCAATTCCAACCCAATTAATTACTACTAATGCTAATAAATCAAGAGAAATCTCAATT    840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AATTCCAATTCCAACCCAATTAATTACTACTAATGCTAATAAATCAAGAGAAATCTCAATT    840

Qy    841 GGAAAAATTTACCTCCATTAATTAAAAGACAATTGGTCGTAATAATTCTAATAATTT    900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GGAAAAATTTACCTCCATTAATTAAAAGACAATTGGTCGTAATAATTCTAATAATTT    900

Qy    901 TGAAAAATGATTTAGTTAGTCCCATGACAAAATGAAAACTAAATGATGATAGTGAAGATATTAC    960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TGAAAAATGATTTAGTTAGTCCCATGACAAAATGAAAACTAAATGATGATAGTGAAGATATTAC    960

Qy    961 TAATACTAGCACCACTGCTAATCATATGAAACTTGGTATTGGTGCTACAACCCTTGGTGT   1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TAATACTAGCACCACTGCTAATCATATGAAACTTGGTATTGGTGCTACAACCCTTGGTGT   1020

Qy   1021 TGGAACTGGTACTACCGGCCACTGCCACTGCCGCCATCTCG   1080
          |||||||||||||||||||||||||||||||||||||||||
Db   1021 TGGAACTGGTACTACCGGCCACTGCCACTGCCGCCATCTCG   1080
```

```
Qy   1081 TTCATCTATTGATAGTGAAGCTGATTCTCATGCATCAAGATCATCTCAAGAAACTGAAGA   1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TTCATCTATTGATAGTGAAGCTGATTCTCATGCATCAAGATCATCTCAAGAAACTGAAGA   1140

Qy   1141 AGATGTTGTTTTCCTAGTGGTGATCATATTGGTGGTAATGGAATTGATTTTGATGA   1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 AGATGTTTGTTTCCTAGTGGTGATCATATTGGTGGTAATGGAATTGATTTTGATGA   1200

Qy   1201 AATTGATGAATTTATTAGAGAAGAAGAGAGCTTATTTACAAAAACAAATGATTGC   1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AATTGATGAATTTATTAGAGAAGAAGAGAGCTTATTTACAAAAACAAATGATTGC   1260

Qy   1261 TAAAAATATTCTGCGTATTGATGAATTCAAAATCTTCCAAAATAATAAAATATACTACTAGTGG   1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TAAAAATATTCTGCGTATTGATGAATTCAAAATCTTCCAAAATAATAAAATATACTACTAGTGG   1320

Qy   1321 TGCATCTCGTCATCCATATCATCATGAATTACTCATGAAAATTCTTCATCTTCAGAAGAAATTATGGATT   1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 TGCATCTCGTCATCCATATCATCATGGCAGCATTCATGAAAATTCTTCATCTTCAGAAGAAATTATGAATT   1380

Qy   1381 TGGTGGGGTTCTAGTTATGGGCAGCCATGTCCGATCTGGGCAGGTGAAAATTGGTGGAG   1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TGGTGGGGTTCTAGTTATGGGCAGCCATGTCCGATCTGGGCAGGTGAAAATTGGTGGAG   1440

Qy   1441 ATTATCAAGATTTGAATTTACTCATGAAAATTCTTCATCTTCAGAAGAAATTTATGAATT   1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ATTATCAAGATTTGAATTTACTCATGAAAATTCTTCATCTTCAGAAGAAATTTATGAATT   1500

Qy   1501 GAAGACTAAACAACAACACCACCTTACAAATGATGATCAATTATCATTCATCTCTAC   1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 GAAGACTAAACAACAACACCACCTTACAAATGATGATCAATTATCATTCATCTCTAC   1560

Qy   1561 ATCTTCTACTTCTGGATCTGGGCAGGTGAAATTTGGTGGAGCAGGTGAAATTTCTGA   1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 ATCTTCTACTTCTGGATCTGGGCAGGTGAAATTTGGTGGAGCAGGTGAAATTTCTGA   1620

Qy   1621 TGGGATTAATGGAGGTTCATTACCTGATAGATTTCACTTTTCCATTCTGAATCAGAAGA   1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TGGGATTAATGGAGGTTCATTACCTGATAGATTTCACTTTTCCATTCTGAATCAGAAGA   1680

Qy   1681 AACTATTCATGCCCCGATATTCATCATTAGTATCCACCAGGTCAATCTGTTCGAGATTT   1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 AACTATTCATGCCCCGATATTCATCATTAGTATCCACCAGGTCAATCTGTTCGAGATTT   1740

Qy   1741 ATTTAGAAATGGTGAAGAACTTGGTGGTGTACTTGTCCTACTGTGATTCGGAAAT   1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 ATTTAGAAATGGTGAAGAACTTGGTGGTGTACTTGTCCTACTGTGATTCGGAAAT   1800

Qy   1801 GAAAATGTTGGCCAAAGCATTGGTATTCATCCTTAACTGCTGAAGATATTCGAATGCA   1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GAAAATGTTGGCCAAAGCATTGGTATTCATCCTTAACTGCTGAAGATATTCGAATGCA   1860

Qy   1861 AGAAACTCGTCAATTGAGAAAAGTTGAATTATTTAAAGTTATTATTTGTTGTTCCATACTTT   1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AGAAACTCGTCAATTGAGAAAAGTTGAATTATTTAAAGTTATTATTTGTTGTTCCATACTTT   1920

Qy   1921 TGAAGCTGATAAAGAAATCGTCGTAATTATTAGACCGATAAATGTTTATTGTTGTTTT   1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TGAAGCTGATAAAGAAATCGTCGTAATTATTAGACCGATAAATGTTTATTGTTGTTTT   1980

Qy   1981 CCATGATGGTATATTAACGTTCCATTTTCTCATCCAGCAAATGTTAGAAG   2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CCATGATGGTATATTAACGTTCCATTTTCTCATCCAGCAAATGTTAGAAG   2040

Qy   2041 AAGAGTTCGTCAATTGAGAGATTATGTCGATTGGTAGTGTCTATGTCCTT   2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AAGAGTTCGTCAATTGAGAGATTATGTCCATGTTAGTGTGCTTATGTGCCTT   2100

Qy   2101 AATCGATGAAATTACCGATGTTTTGCCCCCGTGATTCATGGAATTGAATATGAAGCTGA   2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 AATCGATGAAATTACCGATGTTTTGCCCCCGTGATTCATGGAATTGAATATGAAGCTGA   2160

Qy   2161 TGCCATTGAAGATGCCGTTTTCACTGCTAGAGATACTGATTTTAGTAGTAGTATGTATGTTACAAAG   2220
```

```
Db  3241 TTTATAATTGTATATAATCGTATACTAACTTCTTCTTGATTTAGGGAAGAGTTATATTA 3300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3301 TTTACTATAAACATTTATTTTTACGAGTTGTGTTAAATTGGAGAGTCAAATTAATAGGAT 3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 TTTACTATAAACATTTATTTTTACGAGTTGTGTTAAATTGGAGAGTCAAATTAATAGGAT 3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3361 GTAAAGAAGTTTTAAAGAAGGAATAAAGAAATATTAATTCATACAGAA 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 GTAAAGAAGTTTTAAAGAAGGAATAAAGAAATATTAATTCATACAGAA 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3421 GGGGGGGGAAGGAAGGGGATATATCGGCATTGTGCGTACTTTTGTTTTGAAATA 3480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 GGGGGGGGAAGGAAGGGGATATATCGGCATTGTGCGTACTTTTGTTTTGAAATA 3480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3481 AAATATAAGTTATCTAAATTATTATCAATATTATTATCAATATTGC 3525
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 AAATATAAGTTATCTAAATTATTATCAATATTATTATCAATATTGC 3525
```

```
RESULT 2
AX046919
LOCUS       AX046919                3525 bp    DNA        linear     PAT 15-DEC-2000
DEFINITION  Sequence 3 from Patent WO0068420.
ACCESSION   AX046919
VERSION     AX046919.1  GI:11876349
KEYWORDS
SOURCE      Candida albicans
  ORGANISM  Candida albicans
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE   1  (bases 1 to 3525)
  AUTHORS   Roemer,T., Bussey,H. and Davison,J.
  TITLE     Identification of candida albicans essential fungal specific genes
            and use thereof in antifungal drug discovery
  JOURNAL   Patent: WO 0068420-A 3 16-NOV-2000;
            Mycota Biosciences Inc. (CA)
FEATURES             Location/Qualifiers
     source          1..3525
                     /organism="Candida albicans"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:5476"
     CDS             338..3106
                     /note="unnamed protein product"
                     /codon_start=1
                     /transl_table=12
                     /protein_id="CAC18924.1"
                     /db_xref="GI:11876350"
                     /translation="MSDSESYYQNSTTNQPIPRSDEVLDDHRNQITNDCAISDSEDEL
                     ELKSELESEVVKSEKQQQHQEITSDNAKPLTRKSGSSIKKSNLTDKDRITNPMSLS
                     GGDDTINSGHKNRNYNMSSLRKDFYLKDNTDDNSTNNHTHLAIPIPIPTPIITNAN
                     KSRRKSQLENLPPLIKKKTIGRNNSNNFENDLVSPMTKMKYNDSEDITNTSTANRMK
                     LGIGATTLGVGTGTTATATATAAAGRRPSRSSIDSEADSHASRSSQETEEDVCFPMVG
                     DHIRVNGIDFDEIDEPIREEREEAYLQKOMIAKNISRIDEFQNLSKNNTTSGASRHPY
                     HHHSNNNKKONNGDGDGGGSSWAALKYTPKNILKKTLSRFEFTHENSSSSSEEIYELKTKQ
                     QPPYKYDDQLSLTSSTSSTSSGSGGVKFGGARISDGINGGSLPDRFSLFHSESEETI
                     HAPDIPSLVSPGQSVRDLFRNGEETWWLDCTCPTDSEMKMLAKAFGIHPLTAEDIRMQ
                     ETREKVELFKSYYFVCFHTFRADKSESEDYLEPINVYIVFHDGILTFHFSPISHPANV
                     RRRVRQLRDYVDVSADWLRLLSGKADVIKMFAKCQERANSSSGYYQROYNLQQQOQAP
                     MLQRIGESRRKVMTLMRLLSGKADVIKMFAKCQERANSSSGYYQROYNLQQQOQAP
                     PPPPNPIITSPINSTLNLNSLGTSTGGGVGVGGINFGPNGTWNTNTNTNTTGSPSPP
                     QOQOHGITNKSFPIPDARPRADIALYLGDIQDHIITMFQNLLAYEKIFSRSHSNYLA
                     QLQVESFNSNNKITEMFSKITLIGTMLVPLNLVTGLFGMNVRVPGEGGTNLGWFFGIV
                     GVLIFIIIGSPIFAQWLKKLNNSIEGQNNGNRPIFNHSSRRSIRSLGLKKHGGNKSI
                     ISFPNKYE"
ORIGIN

Query Match             99.9%;  Score 3523;  DB 6;  Length 3525;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 3525;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 TATATAATAATAATATATAAAACATAACATAACATATAAAAAAAAACTTCATATTTCAACTGTT 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 TATATAATAATAATATATAAAACATAACATAACATAACATATAAAAAAAACTTCATATTTCAACTGTT 60
```

(left column sequence alignments, positions 2161–3300)

```
Qy   61 CAACCCAACACCCCCCTGTTCCTAGTCTAGTCCAATTTATTAAGTCATATATGTTGATT 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CAACCCAACACCCCCCTGTTCCTAGTCTAGTCCAATTTATTAAGTCATATATTGTTGATT 120

Qy  121 AATTAAACAGTCACTAGTCCTAGTCCTCAGTCCTCAGTCTTGGTTCTTAATATTAAGA 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 AATTAAACAGTCACTAGTCCTAGTCCTCAGTCCTCAGTCTTGGTTCTTAATATTAAGA 180

Qy  181 TNTTCCATTTTTTTTTTTTTACCCAAGCTATGAAATTATTTTGTTCTAACAACTATA 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TNTTCCATTTTTTTTTTTTTACCCAAGCTATGAAATTATTTTGTTCTAACAACTATA 240

Qy  241 ATAATATTTACCAGAAATGCTACAAATAAATAAATAAATAAATAATAATATTAATAAGA 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ATAATATTTACCAGAAATGCTACAAATAAATAAATAAATAAATAATAATATTAATAAGA 300

Qy  301 GTATATCTCCCCTTTGTTTTTTCTTCCCAGCCATGTCCGATAGTGAAAGTTATTA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GTATATCTCCCCTTTGTTTTTTCTTCCCAGCCATGTCCGATAGTGAAAGTTATTA 360

Qy  361 TCAAAATTCAACTACTAATCAACCTATTCCTAGATCGTAAATCTGGTTCTTCAATTAAATC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 TCAAAATTCAACTACTAATCAACCTATTCCTAGATCGTAAATCTGGTTCTTCAATTAAATC 420

Qy  421 AAATCAAATCACTAATGATTGTGCCATTAGTGATAGTGAAGATGAGTTGGAATTAAAATC 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 AAATCAAATCACTAATGATTGTGCCATTAGTGATAGTGAAGATGAGTTGGAATTAAAATC 480

Qy  481 AGAATTAGAATCAGAAGTTGTAAAAAGCGAAAAACAACAACAACATCATCAAGAGATTAC 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AGAATTAGAATCAGAAGTTGTAAAAAGCGAAAAACAACAACAACATCATCAAGAGATTAC 540

Qy  541 ATCAGATAATGCTAAACCATTGACTCGTAAATCTGGTTCTTCAATTAAGAAAAAATCTAA 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 ATCAGATAATGCTAAACCATTGACTCGTAAATCTGGTTCTTCAATTAAGAAAAAATCTAA 600

Qy  601 TCTTACCGATAAAGATAGAATTACCAACCCTATGAGTTTATCTGGTGGTGATGATACTAT 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 TCTTACCGATAAAGATAGAATTACCAACCCTATGAGTTTATCTGGTGGTGATGATACTAT 660

Qy  661 TAACAGCCGGTCACAAAAATCGTAATTATAACATGACAGTTCATTACGTAAAGATTTTATTT 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 TAACAGCCGGTCACAAAAATCGTAATTATAACATGACAGTTCATTACGTAAAGATTTTATTT 720

Qy  721 AAAAGATAATAACTGACGACAATTCTACTAATAATCATCTCTAATAATCATATCATCCAATTCC 780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 AAAAGATAATAACTGACGACAATTCTACTAATAATCATCTCTAATAATCATATCATCCAATTCC 780

Qy  781 AATTCCAATTCCAACCCAATTATTACTAATGCTAATAAATCAAGAGAAAATCTCAATT 840
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 AATTCCAATTCCAACCCAATTATTACTAATGCTAATAAATCAAGAGAAAATCTCAATT 840

Qy  841 GGAAAATTACCTCCATTAATTAATTAAAAAGAAAAACAATTGGTCGTAATAATTCTAATAATTT 900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 GGAAAATTACCTCCATTAATTAATTAAAAAGAAAAACAATTGGTCGTAATAATTCTAATAATTT 900

Qy  901 TGAAAATGATTTAGTTAGTTAGTCCCATGTCCCATGACAAAAATGAAAACTAATAGTGAAGATATTAC 960
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 TGAAAATGATTTAGTTAGTTAGTCCCATGTCCCATGACAAAAATGAAAACTAATAGTGAAGATATTAC 960

Qy  961 TAATACTAGCACCACTGGTACTACCGGTAATCATATGAAACTTGGTATTGGTGCTACAACCCTTGGTGT 1020
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 TAATACTAGCACCACTGGTACTACCGGTAATCATATGAAACTTGGTATTGGTGCTACAACCCTTGGTGT 1020

Qy 1021 TGGAACTCGGTACTACCGGTGAGCTGATTCTCATGCATCAAGATCATCTCAAGAAACTGAAGA 1080
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 TGGAACTCGGTACTACCGGTGAGCTGATTCTCATGCATCAAGATCATCTCAAGAAACTGAAGA 1080

Qy 1081 TTCATCTATTGATAGTGAAGCTGAATTCTCATGCATCAAGATCATCTCAAGAAACTGAAGA 1140
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 TTCATCTATTGATAGTGAAGCTGAATTCTCATGCATCAAGATCATCTCAAGAAACTGAAGA 1140
```

```
Qy 1141 AGATGTTTGTTTCCTATGGTTGGTGATCATATTAGAGTTAATGGAATTGATTTTGATGA 1200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 AGATGTTTGTTTCCTATGGTTGGTGATCATATTAGAGTTAATGGAATTGATTTTGATGA 1200

Qy 1201 AATTGATGAATTATTAGAGAAGAAGAAGAAGAAGCTTATTTACAAAAACAAATGATTGC 1260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 AATTGATGAATTATTAGAGAAGAAGAAGAAGAAGCTTATTTACAAAAACAAATGATTGC 1260

Qy 1261 TAAAAATATTCTGCGTATTGATGAATTTCAAAAATCTTCAAAATAATAATACTACTAGTGG 1320
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 TAAAAATATTCTGCGTATTGATGAATTTCAAAAATCTTCAAAATAATAATACTACTAGTGG 1320

Qy 1321 TGCATCTCGTCATCCATATCATCATCACAGTAATAATAATAAAAAAATATTTAAAGAAAAC 1380
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 TGCATCTCGTCATCCATATCATCATCACAGTAATAATAATAAAAAAATATTTAAAGAAAAC 1380

Qy 1381 TGGTGGTGGTTCTAGTATGGCAGCATTAAAATATACTCCAAAAAAATATTTCATCTTCAGAGAAATTTATGAATT 1440
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1381 TGGTGGTGGTTCTAGTATGGCAGCATTAAAATATACTCCAAAAAAATATTTCATCTTCAGAGAAATTTATGAATT 1440

Qy 1441 ATTATCAAGATTGAATTTACTCATGAATAATTCTTCATCTTCAGAGAAATTTCATCTTCAGAGAAGATTTCATCTAC 1500
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1441 ATTATCAAGATTGAATTTACTCATGAATAATTCTTCATCTTCAGAGAAATTTCATCTTCAGAGAAGATTTCATCTAC 1500

Qy 1501 GAAGACTAAACACAACCACCTTACAAATGATCAATTATCATTAACTTCATCTCAC 1560
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1501 GAAGACTAAACACAACCACCTTACAAATGATCAATTATCATTAACTTCATCTCTAC 1560

Qy 1561 ATCTTCTACTTCTGGATCTCTGGATCTCGGGCAGGTGAAATTTGGTGAGCAAGAATTTCTGA 1620
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1561 ATCTTCTACTTCTGGATCTCTGGATCTCGGGCAGGTGAAATTTGGTGAGCAAGAATTTCTGA 1620

Qy 1621 TGGGATTAATGGAGGTTCATTACCTGATAGATTTTCACTTTTCACTTTTCCATTCTGAATCAGAAGA 1680
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1621 TGGGATTAATGGAGGTTCATTACCTGATAGATTTTCACTTTTCACTTTTCCATTCTGAATCAGAAGA 1680

Qy 1681 AACTATTCATGCCCCCGATATTCATCATTAGTATCACCAGGTCAATCTGTTCGAGATTT 1740
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1681 AACTATTCATGCCCCCGATATTCATCATTAGTATCACCAGGTCAATCTGTTCGAGATTT 1740

Qy 1741 ATTTAGAAATGGTGAAGAAACTTGGTGGTGGTTAGATTGTACTTGTCCTACTGATTCGGAAAT 1800
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1741 ATTTAGAAATGGTGAAGAAACTTGGTGGTGGTTAGATTGTACTTGTCCTACTGATTCGGAAAT 1800

Qy 1801 GAAAATGTTGGCCAAAGCATTTGGTATTCATCCTTAACTGCTGAAGATATTCGAATGCA 1860
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1801 GAAAATGTTGGCCAAAGCATTTGGTATTCATCCTTAACTGCTGAAGATATTCGAATGCA 1860

Qy 1861 AGAAACTCGTGAAAAAGTTGAATTATTTAAAAGTTATTATTTGTTTGTTTGTTCCATACTTT 1920
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1861 AGAAACTCGTGAAAAAGTTGAATTATTTAAAAGTTATTATTTGTTTGTTTGTTCCATACTTT 1920

Qy 1921 TGAAGCTGATAAAGAATCTGAAGATTATTTAGAACCGATAAATGTTTATATTGTTGTTTT 1980
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1921 TGAAGCTGATAAAGAATCTGAAGATTATTTAGAACCGATAAATGTTTATATTGTTGTTTT 1980

Qy 1981 CCATGATGCTATATTAACGTTCCATTTTCTCATCCAGCAAATTTCTCATCCAGCAAATGTTAGAAG 2040
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1981 CCATGATGCTATATTAACGTTCCATTTTCTCATCCAGCAAATTTCTCATCCAGCAAATGTTAGAAG 2040

Qy 2041 AAGAGTTCGTCAATTGAAGAATTGAAGAGATTATGTCGATGTTAGTGCTGAATGCA 2100
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2041 AAGAGTTCGTCAATTGAAGAATTGAAGAGATTATGTCGATGTTAGTGCTGAATGCA 2100

Qy 2101 AATGCATGAAATTACCGACGGTTTTCATGGAATTCATGGAATTGAAGATGAAGGCTGA 2160
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2101 AATCGATGAAATTACCGACGGTTTTCATGGAATTCATGGAATTGAAGATGAAGGCTGA 2160

Qy 2161 TGCCATTGAAGATGCCGTTTTCACTGCTAGAGATACTGATTTTTAGTGATGTTACAAAAG 2220
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2161 TGCCATTGAAGATGCCGTTTTCACTGCTAGAGATACTGATTTTTAGTGATGTTACAAAAG 2220

Qy 2221 AATTGGTGAATCAAGAAGAAAAGTCATGACTTTAATGAGATTATTATCAGGTAAAGCTGA 2280
```

```
Db            |||||||||||||||||||||||||
         2221 AATTGGTGAATCAAGAGAAGAAAGTCATGACACTTTAATGAGATTATTCAGGTAAAGCTGA 2280

Qy       2281 TGTCATTAAAAATGTTTGCTAAAAGAGTGTCAAGAGAGAAGCTAATTCTTCTTCTGGTTATTA 2340
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TGTCATTAAAAATGTTTGCTAAAAGAGTGTCAAGAGAGAAGCTAATTCTTCTTCTGGTTATTA 2340

Qy       2341 TCAACGTCAATATAACTTACAACACAACAACAACAGGCCCACCACCACCACCTAATCC 2400
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TCAACGTCAATATAACTTACAACAACAACAACAACAGGCCCACCACCACCACCTAATCC 2400

Qy       2401 TATTATTACTTCACCAATAATTCAACTTTGAATCTTAATAGTTTAGGAACTTCAACTGG 2460
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 TATTATTACTTCACCAATAATTCAACTTTGAATCTTAATAGTTTAGGAACTTCAACTGG 2460

Qy       2461 TGGAGGAGTAGGAGGAGGAATTAATTTGGTCCCAATCCAACTGGAAATAATAACTAA 2520
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 TGGAGGAGTAGGAGGAGGAATTAATTTTGGTCCCAATCCAACTGGAAATAATAACTAA 2520

Qy       2521 TACTAATACTAATACTACTGGTCACCTTCACCTTCACCACCTCAACAACAACAACATGGTAT 2580
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 TACTAATACTAATACTACTGGTCACCTTCACCTTCACCACCTCAACAACAACAACATGGTAT 2580

Qy       2581 CACTAACACAAATCTTTCCCCATCCCCGATGCAGTCCAAGAGCTGATATTGCATTATATTT 2640
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 CACTAACACAAATCTTTCCCCATCCCCGATGCAGTCCAAGAGCTGATATTGCATTATATTT 2640

Qy       2641 AGGTGATATTCAAGATCATCATAATCACCATGTTCAAAATTTATTAGCCTATGAAAAAAT 2700
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 AGGTGATATTCAAGATCATCATAATCACCATGTTCAAAATTTATTAGCCTATGAAAAAAT 2700

Qy       2701 TTTCAGTCGTTCACATTCAAATTATTAGTCAATTACAAGTTGAATCATTCAATTCCAA 2760
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 TTTCAGTCGTTCACATTCAAATTATTAGTCAATTACAAGTTGAATCATTCAATTCCAA 2760

Qy       2761 TAATAAAATCACCGAAAATGTTTCTAAAATTACTTGATTGGGACAAATGTTAGTTCCATT 2820
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 TAATAAAATCACCGAAAATGTTTCTAAAATTACTTGATTGGGACAAATGTTAGTTCCATT 2820

Qy       2821 AAATTTAGTCACGGGACTTTTTGGTATGAATGTAAGAGTCCCTGGTGAAGGTGGTACCAA 2880
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 AAATTTAGTCACGGGACTTTTTGGTATGAATGTAAGAGTCCCTGGTGAAGGTGGTACCAA 2880

Qy       2881 TTTTAGGTTGGTTTTTCGGAATTGTTGGAGTATTATAATTATTGGATCATTTAT 2940
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 TTTTAGGTTGGTTTTTCGGAATTGTTGGAGTATTATAATTATTGGATCATTTAT 2940

Qy       2941 ATTTGCTCAATGGTTGGTTGAAAAAATTGAATAAATCAATTGAAGGACAAAATAATGGTAA 3000
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 ATTTGCTCAATGGTTGGTTGAAAAAATTGAATAAATCAATTGAAGGACAAAATAATGGTAA 3000

Qy       3001 TCGACCAATTTTAATCATTCATCAAGAAGATCAAGAAGTTTAGGTTTAAAAAAAACA 3060
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 TCGACCAATTTTAATCATTCATCAAGAAGATCAAGAAGTTTAGGTTTAAAAAAAACA 3060

Qy       3061 TGGTGGTAATAAATCAATTATTAGTTTCCCCAATAAATAAATATGGAATAAGAATAATCAAAGAA 3120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TGGTGGTAATAAATCAATTATTAGTTTCCCCAATAAATAAATATGGAATAAGAATAATCAAAGAA 3120

Qy       3121 ATGCCACAGAGTTTGATGGTTTGTTTTGTTTTATTGTCATGATGGAGTTGTATAT 3180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 ATGCCACAGAGTTTGATGGTTTGTTTTGTTTTATTGTCATGATGGAGTTGTATAT 3180

Qy       3181 ACATATACTTTTATAGAAGTAACAATAGTAGTAGTCATCAATCATCATA 3240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 ACATATACTTTTATAGAAGTAACAATAGTAGTAGTCATCAATCATCATA 3240

Qy       3241 TTTATATTGTATATAATCGTATACTACAACTTCTTCTTGATTTGAGTTAGGGAAAGAGTTATATTA 3300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 TTTATAATTGTATATAATCGTATACTACAACTTCTTCTTGATTTGAGTTAGGGAAAGAGTTATATTA 3300

Qy       3301 TTTACTATAAACATTTATTTTTACGAGTTGTGTTAAAATTGGAGAGTCAAATTAATAGGAT 3360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 TTTACTATAAACATTTATTTTTACGAGTTGTGTTAAAATTGGAGAGTCAAATTAATAGGAT 3360

Qy       3361 GTAAAAGAAGTTTTAAAGAAGGAATAAAGAAATATTATAATTCAGANGTTCATACAGAA 3420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 GTAAAAGAAGTTTTAAAGAAGGAATAAAGAAATATTATAATTCAGANGTTCATACAGAA 3420

Qy       3421 GGGGGGGAGGAGGAGGGGATATATATCGGCATTTGTGTACTTTGTTTTTGAAATA 3480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GGGGGGGAGGAGGAGGGGATATATATCGGCATTTGTGTACTTTGTTTTTGAAATA 3480

Qy       3481 AAATATAAGTTATCTAAAATTATTATTATCAATTATTATCAATATTGC 3525
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 AAATATAAGTTATCTAAAATTATTATTATCAATTATTATCAATATTGC 3525
```

RESULT 3
```
LOCUS        AX489375                2769 bp    DNA        linear    PAT 16-AUG-2002
DEFINITION   Sequence 6675 from Patent WO02053728.
ACCESSION    AX489375
VERSION      AX489375.1  GI:22323387
KEYWORDS
SOURCE       Candida albicans
  ORGANISM   Candida albicans
             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
             Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE    1
  AUTHORS    Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
  TITLE      Gene disruption methodologies for drug target discovery
  JOURNAL    Patent: WO 02053728-A 6675 11-JUL-2002;
             Elitra Pharmaceuticals, Inc. (US)
FEATURES     Location/Qualifiers
  source     1..2769
             /organism="Candida albicans"
             /mol_type="unassigned DNA"
             /db_xref="taxon:5476"
ORIGIN

Query Match     78.6%;  Score 2769;  DB 6;  Length 2769;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 2769;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
```

```
Qy        338 ATGTCCGATAGTGAAAGTTATTATCAAAATTCAACTAATCAACCTAATCAACCTATTCCTAGATCT 397
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCCGATAGTGAAAGTTATTATCAAAATTCAACTAATCAACCTAATCAACCTATTCCTAGATCT 60

Qy        398 GATGAAGTATTGGATGATCATAGAATCAAATCAAATCAGAATCAAGAAGTGTGCCATTAGTGTGATAGT 457
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGAAGTATTGGATGATCATAGAATCAAATCAAATCAGAATCAAGAAGTGTGCCATTAGTGTGATAGT 120

Qy        458 GAAGATGAGTGGAATTAAAATCAGAATCAGAAGTTGTAAAAGCGAAAAACAA 517
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAGATGAGTGGAATTAAAATCAGAATCAGAAGTTGTAAAAGCGAAAAACAA 180

Qy        518 CAACAACATCATCAAGAGATTACATCAGAATAATGCTAAACCATTGACTCGGTAAATCTCGGT 577
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAACAACATCATCAAGAGATTACATCAGAATAATGCTAAACCATTGACTCGGTAAATCTGGT 240

Qy        578 TCTTCAATTAAGAAAAATCTAATCTTACCGATAAAGATAGAATTACCAACCCTATGAGT 637
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTTCAATTAAGAAAAATCTAATCTTACCGATAAAGATAGAATTACCAACCCTATGAGT 300

Qy        638 TTATCTGGTGGTGATGATCATATTAACAGCGGTCACAAAATCGTAATTATAACATGAGT 697
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTATCTGGTGGTGATGATCATATTAACAGCGGTCACAAAATCGTAATTATAACATGAGT 360

Qy        698 TCATTACGTAAAGATTTTATTAAAAGATAATAATCGACGACAATTCTACTAATAATCAT 757
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCATTACGTAAAGATTTTATTAAAAGATAATAATCGACGACAATTCTACTAATAATCAT 420

Qy        758 ACTCATCTTCGAATTCCAATTCCAACCCCAATTCCAATTATTACTACTGTAAT 817
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACTCATCTTCGAATTCCAATTCCAACCCCAATTCCAATTATTACTACTGTAAT 480
```

Fri Apr 15 11:05:58 2005   us-10-018-105-3.rge

```
Qy    818 AAATCAAGAAGAAATCTCAATTGGAAAATTACCTCCATTAATTAAAAGAAAACAATT 877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AAATCAAGAAGAAATCTCAATTGGAAAATTACCTCCATTAATTAAAAGAAAACAATT 540

Qy    878 GGTCGTAATAATTCTAATAATTTGAAAATGATTTAGTTAGTTAGTTCCCATGACAAAATGAAA 937
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGTCGTAATAATTCTAATAATTTGAAAATGATTTAGTTAGTTAGTTCCCATGACAAAATGAAA 600

Qy    938 ACTAATGATAGTGAAGATATTACTAATACTAGCACCACTGCTAATCATATGAAACTTGGT 997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ACTAATGATAGTGAAGATATTACTAATACTAGCACCACTGCTAATCATATGAAACTTGGT 660

Qy    998 ATTGGTGCTACAACCCTTGGTGTTGGAACTGGTACTACCGCCACTGCCACTGCT 1057
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ATTGGTGCTACAACCCTTGGTGTTGGAACTGGTACTACCGCCACTGCCACTGCT 720

Qy   1058 GCTGCTGGTAGGAGACCATCTCGTTCATTCATTGATAGTGAAGCTGAATTCATGCATCA 1117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GCTGCTGGTAGGAGACCATCTCGTTCATTCATTGATAGTGAAGCTGAATTCATGCATCA 780

Qy   1118 AGATCATCTCAAGAAACTGAAGAAGAAGATGTTTGTTTTCCTATGGTTGGTGATCATATTAGA 1177
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AGATCATCTCAAGAAACTGAAGAAGAAGATGTTTGTTTTCCTATGGTTGGTGATCATATTAGA 840

Qy   1178 GTTAATGGAATTGATTTTGATGAAATTGATGAAATTGATTTATTAGAGAAGAAGAAGAAGCT 1237
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GTTAATGGAATTGATTTTGATGAAATTGATGAAATTGATTTATTAGAGAAGAAGAAGAAGCT 900

Qy   1238 TATTTACAAAAAACAAATGATTGCTAAAAATATTCTGCGTATTGTTAAAAATATTCAAAATCTT 1297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TATTTACAAAAAACAAATGATTGCTAAAAATATTCTGCGTATTGTTAAAAATATTCAAAATCTT 960

Qy   1298 TCCAAAAATAATTACTACTAGTGGTGCATCTCGTCATCCATATCATCAGTAATAAT 1357
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCCAAAAATAATTACTACTAGTGGTGCATCTCGTCATCCATATCATCAGTAATAAT 1020

Qy   1358 AATAAAAAAATATTTTAAAGAAAACATTATCAAGATTGAATTTACTCAAGAAAATTCTTCA 1417
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AATAAAAAAATATTTTAAAGAAAACATTATCAAGATTGAATTTACTCAAGAAAATTCTTCA 1080

Qy   1418 CCAAAAAATATTTTAAAGAAACATTATCAAGATTTGAATTTGAAATTCAAGAAAATTCTTCA 1477
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CCAAAAAATATTTTAAAGAAACATTATCAAGATTTGAATTTGAAATTCAAGAAAATTCTTCA 1140

Qy   1478 TCTTCAGAAGAAATTATTGAAGACTAAACAACAACCACCTTACTCTGAATCTGGATCTGATGAT 1537
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCTTCAGAAGAAATTATTGAAGACTAAACAACAACCACCTTACTCTGAATCTGGATCTGATGAT 1200

Qy   1538 CAATTATCATTAACTTCATCTACATCTTCTACTTCTGGATTAATGGAGGTTCATTACCTGATGAAATG 1597
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CAATTATCATTAACTTCATCTACATCTTCTACTTCTGGATTAATGGAGGTTCATTACCTGATGAAATG 1260

Qy   1598 TTTTGGTGGAGCAAGAATTCTGATGGGATTAATGGAGGTTCATTACCTGATGAGATTTCA 1657
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TTTTGGTGGAGCAAGAATTCTGATGGGATTAATGGAGGTTCATTACCTGATGAGATTTCA 1320

Qy   1658 CTTTTTCCATTCTGAATCAGAAGAAACTATTCATGCCCCCGATAATTCCATCATTAGTATCA 1717
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 CTTTTTCCATTCTGAATCAGAAGAAACTATTCATGCCCCCGATAATTCCATCATTAGTATCA 1380

Qy   1718 CCAGGTCAATCTCGTTCGAGATTTATTTAGAAGAAACTGGTGGTGTTAGATTGT 1777
          |||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   1381 CCAGGTCAATCTGTTCGAGATTTATTTAGAAGAAACTGGTGGTGTTAGATTGT 1440

Qy   1778 ACTTGTCCTACTACTTCATCTACATCTTCATCTACATCTTGGTATTCATCCTTTA 1837
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ACTTGTCCTACTACTTCATCTACATCTTCATCTACATCTTGGTATTCATCCTTTA 1500

Qy   1838 ACTGCTGAAGATATTCGAATCGAAGAAACTCGTGAAGAACTCGTGAAAAAGTTAT 1897
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 ACTGCTGAAGATATTCGAATCGAAGAAACTCGTGAAGAACTCGTGAAAAAGTTAT 1560


Qy   1898 TATTTGTTTGTTTGTTTCCATACTTTGAAGCTGATAAAGAAATCTGAAGATTATTTAGAACCG 1957
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TATTTGTTTGTTTGTTTCCATACTTTGAAGCTGATAAAGAAATCTGAAGATTATTTAGAACCG 1620

Qy   1958 ATAAATGTTTATATTGTTGTTTCCATGATGGTATATTAACGTTCCATTTTTCACCAATT 2017
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 ATAAATGTTTATATTGTTGTTTCCATGATGGTATATTAACGTTCCATTTTTCACCAATT 1680

Qy   2018 TCTCATCCAGCAAATGTTAGAAGAAGAGTTCGTCAATTGAGAGATTATGTCGATGTTAGT 2077
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TCTCATCCAGCAAATGTTAGAAGAAGAGTTCGTCAATTGAGAGATTATGTCGATGTTAGT 1740

Qy   2078 GCTGATTGGTTATGTTATGTGTTAATCGATGAAATTACCGATGGTTTTGCCCCGTGATT 2137
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCTGATTGGTTATGTTATGTGTTAATCGATGAAATTACCGATGGTTTTGCCCCGTGATT 1800

Qy   2138 CATGGAATTGAATATGAAGCTGAAGCTGATGCCATTGAAGATGCCGTTTCACTGCTAGAGATACT 2197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CATGGAATTGAATATGAAGCTGAAGCTGATGCCATTGAAGATGCCGTTTCACTGCTAGAGATACT 1860

Qy   2198 GATTTTAGTAGTATGTTACAAAGAATTGGTGAATCAAGAGAAGAAAGTCATGACTTTAATG 2257
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 GATTTTAGTAGTATGTTACAAAGAATTGGTGAATCAAGAGAAGAAAGTCATGACTTTAATG 1920

Qy   2258 AGATTATTATCAGGTAAAGCTAAAGTGTCATTAAAATGTTGCTAAAAGATGTCAAGAAGAA 2317
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 AGATTATTATCAGGTAAAGCTAAAGTGTCATTAAAATGTTGCTAAAAGATGTCAAGAAGAA 1980

Qy   2318 GCTAATTCTTCTTCTCGGTTATTATCAACGTCAATATAACTTACCAATTAATTCAACTTTGAATCTT 2377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 GCTAATTCTTCTTCTCGGTTATTATCAACGTCAATATAACTTACCAATTAATTCAACTTTGAATCTT 2040

Qy   2378 GCCCCACCACCACCTAATCCTATTATTACTTCACCAATTAATTACTTCACCAATTAATTCAACCT 2437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 GCCCCACCACCACCTAATCCTATTATTACTTCACCAATTAATTACTTCACCAATTAATTCAACCT 2100

Qy   2438 AATAGTTTAGGAACTTCAACTGGTGGAGTAGGAGTAGGAGGAATTAATTTTGGTCCC 2497
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 AATAGTTTAGGAACTTCAACTGGTGGAGTAGGAGTAGGAGGAATTAATTTTGGTCCC 2160

Qy   2498 AATCCAACTGGAAATAATAATACTAATACTAATCTTTCCCATCCCGATCGCACGTCCA 2557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 AATCCAACTGGAAATAATAATACTAATACTAATCTTTCCCATCCCGATCGCACGTCCA 2220

Qy   2558 CAACAACAACAACAACATGTATCACTAACAACAAATCTTCCCATCCCGATGCGACGTCCA 2617
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CAACAACAACAACAACATGTATCACTAACAACAAATCTTCCCATCCCGATGCGACGTCCA 2280

Qy   2618 AGAGCTGATATTGCATTATATTGGTGATATTCAAGATCAATAATCACCATGTTTCAA 2677
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 AGAGCTGATATTGCATTATATTGGTGATATTCAAGATCAATAATCACCATGTTTCAA 2340

Qy   2678 AATTTATTAGCCTATGAAAAATTTCAGTCGTTCACATTCAATTATTTAGCTCAATTA 2737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATTTATTAGCCTATGAAAAATTTCAGTCGTTCACATTCAATTATTTAGCTCAATTA 2400

Qy   2738 CAAGTTGAATCATTCAATTCAATATAAATCACCGAAATGTTTTCTAAAATTACTTTG 2797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 CAAGTTGAATCATTCAATTCAATATAAATCACCGAAATGTTTTCTAAAATTACTTTG 2460

Qy   2798 ATTGGGACAATGTTAGTTCATTCATTAAATTTAGTCACGGGACTTTTTGGTATGAATGTAAGA 2857
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 ATTGGGACAATGTTAGTTCATTCATTAAATTTAGTCACGGGACTTTTTGGTATGAATGTAAGA 2520

Qy   2858 GTCCCTGGTGAAGGTGGTACCAATTTAGGTTCGGTTTTTCGGAATTGTTGGAGTATTAATA 2917
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 GTCCCTGGTGAAGGTGGTACCAATTTAGGTTCGGTTTTTCGGAATTGTTGGAGTATTAATA 2580

Qy   2918 TTTATAATTATTGGATCATTTATATTTTGCTCAATGGTGTTGAAAAAATTGAATAATTCA 2977
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTTATAATTATTGGATCATTTATATTTTGCTCAATGGTGTTGAAAAAATTGAATAATTCA 2640

Qy   2978 ATTGAAGGACAAAATAATGGTAATCACCAATTTTAATCATTCAAGAAGATCAATT 3037
```

us-10-018-105-3.rge

Apr 15 11:05:58 2005

```
Db   2641 ATTGAAGGACAAAAATAATGGTAATCGACCAATTTTAATCATTCATCAAGAGAGATCAATT 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3038 AGAAGTTTAGGTTAAAAAAACATGGTGGTAATAAATCAATTATTAGTTTCCCCAATAAA 3097
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2701 AGAAGTTTAGGTTAAAAAAACATGGTGGTAATAAATCAATTATTAGTTTCCCCAATAAA 2760

Qy   3098 TATGAATAA 3106
          |||||||||
Db   2761 TATGAATAA 2769
```

```
RESULT 4
AR551197
LOCUS       AR551197              2358 bp    DNA        linear      PAT 08-OCT-2004
DEFINITION  Sequence 6328 from patent US 6747137.
ACCESSION   AR551197
VERSION     AR551197.1  GI:5394372
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2358)
  AUTHORS   Weinstock,K.G. and Bush,D.
  TITLE     Nucleic acid sequences relating to Candida albicans for diagnostics
            and therapeutics
  JOURNAL   Patent: US 6747137-A 6328 08-JUN-2004;
FEATURES             Location/Qualifiers
     source          1..2358
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match             61.1%;  Score 2155.2;  DB 6;  Length 2358;
Best Local Similarity   97.2%;  Pred. No. 4e-292;
Matches 2293;  Conservative     0;  Mismatches   23;  Indels  44;  Gaps  8;
```

```
Qy    285 ATAAATATAATTAAGAGTATATCTCCCCTTTGTTTTTTTTTCTTCCCAGCCATGTCCG 344
          |||||||||||||||||||||||||||||||| ||||  | |||||||||||||||||
Db      1 ATAAATATAATTAAGAGTATATCTCCCCTTTG---TTTTTTTTCTTCCCAGCCATGTCCG 58

Qy    345 ATAGTGAAAGTATTATTCAACTACTAACTCAAATTCAACCTATTCCTAGATCTGATGAAG 404
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     59 ATAGTGAAAGTATTATTCAACTACTAACTCAAATTCAACCTATTCTTAGATCTGATGAAG 118

Qy    405 TATTGGATGATCATAGAAAATCAAATCAAATCAATAATGATTGTGCCATTAGTGATAGTGAAGAATG 464
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    119 TATTGGATGATCATAGAAAATCAAATCAAATCAATAATGATTGTGCCATTAGTGATAGTGAAGAATG 178

Qy    465 AGTTGGAATTAAAATCAGAATTAGAATCAGAAGTTGTAAAAAGCGAAA------T 512
          |||||||||||||||||||||||||||||||||| ||||||
Db    179 AGTTGGAATTAAAACCAGAATTAGAATCAGAAGTTGCAAAAAGCGAAAAACAACAACAC 238

Qy    513 AACAACAACAACATCATCATCAAGAGATTACATCAGATAAATGCTAAACCATTGACTCGTAAAT 572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    239 AACAACAACAACATCATCATCAAGAGATTACATCAGATAAATGCTAAACCATTGACTCGTAAAT 298

Qy    573 CTGGTTCTTCAATTAAGAAAAATCTAATCTTACCGATAAAGATAGAATTACCACCCCTA 632
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    299 CTGGTTCTTCAATTAAGAAAAATCTAATCTTACCGATAAAGATAGAATTACCACCCCTA 358

Qy    633 TGAGTTTATCTCGTGGTGGTGATGATCTATTAACAGCGGTCACAAAAATCGTAATTATAACA 692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    359 TGAGTTTATCTCGTGGTGGTGATGATCTATTAACAGCGGTCACAAAAATCGTAATTATAACA 418

Qy    693 TGAGTTCATTACGTAAAGATTTTATTTAAAAGATAATACTGACGACAATTCTACTAATA 752
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    419 TGAGTTCATTACGTAAAGATTTTATTTAAAAGATAATACTGACGACAATTCTACTAATA 478

Qy    753 ATCATACTCATCTTGCAATTCCAATTCCAATTCCAACCCCAATTATTACTAATG 812
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    479 ATCATACTCATCTTGCAATTCCAATTCCAATTCCAACCCCAATTATTACTAATG 538
```

```
Qy    813 CTAATAAATCAAGAAGAGAAATCTCAATTGGAAAATTTACCTCCATTAATTAAAAGAAAA 872
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    539 CTAATAAATCAAGAAGAGAAATCTCAATTGGAAAATTTACCTCCATTAATTAAAAGAAAA 598

Qy    873 CAATTGGTCGTAATAATCTAATAATTTGAAAATGATTAGTTAGTTAGTTCCCATGACAAAAA 932
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    599 CTATTGGTCGTAATAATCTAATAATTTGAAAATGATTAGTTAGTTAGTTCCCATGACAAAAA 658

Qy    933 TGAAAACTAATGATAGTGAAGATATTACTAA---TACTAGCACCACTGCTAATCATATGA 989
          |||||||||||||||||||||||||||||          |||||||||||||||||||
Db    659 TGAAAACTAATGATAGTGAAGATATTACTAACTACTAGCACTAGCACCACTGCTAATCATATGA 718

Qy    990 AACTTGGTATTGGTGCTACAACCCTTGGTGTTGGAACGTGGTACTACCGCCACTGCCACTG 1049
          ||||||||||||||||||||||||       ||||||||||||||||||||||||||||
Db    719 AACTTGGTATTGGTGCTACAACCCTTGGTGTTGGAACGTGGTACTACCGCCACTGCCACTG 778

Qy   1050 CCACTGCTGCTGC-------TGGTAGAAGACCATCTCGTTCATTGATAGTGAAG 1100
          ||||||||||                 |||||||||||||||||||||||||
Db    779 CCACTGCTACTGCTGGTGGTGGTGGTGGTAGAAGACCATCTCGTTCATTGATAGTGAAG 838

Qy   1101 CTGATTCTCATGCATCAAGATCATCTCAAGAAACTCGAAGAAGATGTTTGTTTTCCTATGG 1160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    839 CTGATTCTCATGCATCAAGATCATCTCAAGAAACTCGAAGAAGATGCTTGTTTTCCTATGG 898

Qy   1161 TTGGTGATCATATTAGAGTTAATGGAATTGAATTGAATTTGATGAATTTGATGAATTTATTAGAG 1220
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    899 TTGGTGATCATATTAGAGTTAATGGAATTGAATTGAATTTGATGAATTTGATGAATTTATTAGAG 958

Qy   1221 AAGAAAGAGAAGAAGCTTATTTACAAAACAAATGATTGCTAAAAATATTCTGCGTATTG 1280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    959 AAGAAAGAGAAGAAGCTTATTTACAAAACAAATGATTGCTAAAAATATTCTGCGTATTG 1018

Qy   1281 ATGAATTTCAAAATCTTCAAAATAATATACTACTAGTGGTGCATCTCGTCATCCCATATC 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1019 ATGAATTTCAAAATCTTCAAAATAATATACTACTAGTGGTGCATCTCGTCATCCCATATC 1078

Qy   1341 ATCATCACAGTAATAATAATAAAAAAAAAATAATGATG---GTGGTCGGTTCTAGTA 1397
          |||||||||||||||||||||||||||||||||||||   ||||||||||||||
Db   1079 ATCATCACAGTAATAATAATAAAAAAAATAATAATGGTGGTGATGGTGAGTGGTTCTAGTA 1138

Qy   1398 TGGCAGCATTAAAATATACTCCAAAAATATTTAAAGAAAACATTATCAAGATTTGAAT 1457
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1139 TGGCAGCATTAAAATATACTCCAAAAATATTTAAAGAAAACATTATCAAGATTTGAAT 1198

Qy   1458 TTACTTCATGAAAATTCTTCATCTTCAGAAGAAATTTATGAATTTATGAATTCAACAACAAC 1517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1199 TTACTTCATGAAAATTCTTCATCTTCAGAAGAAATTTATGAATTTATGAATTCAACAACAAC 1258

Qy   1518 CACCTTACAAATATGATGATCAATTATCATTAACTTCATCGTCACTACATCTTCTACT------T 1571
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1259 CACCTTACAAATATGATGATCAATTATCATTAACTTCATCATCACTACATCTTCTACTTCTGGAT 1318

Qy   1572 CTGGATCTCGGATCTCGGGCAGGTGAAATTTCTGATGGGATTAATG 1631
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1319 CTGGATCTCGGATCTCGGGCAGGTGAAATTTCTGATGGGATTAATG 1378

Qy   1632 GAGGTTCATTACCTGATAGATTTCACTTTTCCATTCTGAATCAGAAGAAACTATTCATG 1691
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1379 GAGGTTCATTACCTGATAGATTTCACTTTTCCATTCTGAATCAGAAGAAACTATTCATG 1438

Qy   1692 CCCCGATATTCATCATAGTATCACCAGGTCAAAAATCGTAATTATTAGAAATG 1751
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1439 CCCCGATATTCATCATCATAGTATCACCAGGTCAAAAATCGTAATTATTAGAAATG 1498

Qy   1752 GTGAAGAAACTTGGTTGGGTTAGATTGTTACTTGTCCTACTGATTCGGAAATGAAATGTTGG 1811
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1499 GTGAAGAAACTTGGTTGGGTTAGATTGTTACTTGTCCTACTGATTCGGAAATGAAATGTTGG 1558

Qy   1812 CCAAAGCATTTGGTATTCATCCTTTAACTGCTGAAGATATTCGAATGCAAGAAACTCGTG 1871
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1559 CCAAAGCATTTGGTATTCATCCTTTAACTGCTGAAGATATTCGAATGCAAGAAACTCGTG 1618

Qy   1872 AAAAAGTTGAATTATTTAAAAGTTATTATTTTGTTTGTTTCCATACTTTTGAAGCTGATA 1931
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
CR382138_16                    1600001   1710000
CR382138_17                    1700001   1810000
CR382138_18                    1800001   1910000
CR382138_19                    1900001   2010000
CR382138_20                    2000001   2110000
CR382138_21                    2100001   2210000
CR382138_22                    2200001   2310000
CR382138_23                    2300001   2336804

Continuation (15 of 24) of CR382138 from base 1400001 (CR382138 Debaryomyces hansenii ch

Query Match      16.5%;   Score 581;  DB 8;  Length 110000;
Best Local Similarity   58.1%;   Pred. No. 1.9e-72;
Matches 1348;   Conservative   0;   Mismatches 815;   Indels 158;   Gaps   12;


Qy  1067 AGAAGACCATCTCGTTCATCTATTGATAGTGAGCTGATTCTCATGCATCAAGATCATCT 1126
         |||||| |||||||||||  ||||| ||||||| |||||| ||||||  |||||
Db 14194 AGAAGACCATCCCGTACTTCAATAGATACGGAGCATGCGTCCGAGTCGAGTCTTCA 14135

Qy  1127 CAAGAAACTGAAGAAGATGTTTGTTTCCTATGGTGGTGATCATATTAGAGTTAATGA 1186
         |||||| |||||||||| |||||||||||||| |||||||||| |||| |||||||
Db 14134 CAGGAGACAGAAGAGATGTTTCCTTTCCTATGTGCGTGAACACGTTCGTGTTAAGGGT 14075

Qy  1187 ATTGATTTTGATGAAATTGATGAAATTGAAGAGTTCATTAGA--AGAAAGAGAAGAAGCTTATTAC 1244
         ||||||||||||||||||||||||||||||| ||||||||  |||||||| |||| |||||
Db 14074 ATTGATTTTGATGAAATTGATGAAATTGAAGAGTTCATTAGAGATGAGAAAAGAGAATGAAATGCATTTA 14015

Qy  1245 AAAAACAAATGATTGCTAAAAATATTCTCGTATTGATGATTGATGAAATCTTTCAAAA 1304
         ||||||||||||||||||||||||| ||||||||||||||||
Db 14014 AAAGAGGAACAACAGATGATCGCGCAGAAAGAACACAGCCATGAGGGT-----TGATACTGGAC 13960

Qy  1305 ATAATACTACTAGTTGGTGCATCTCGTCATCCATATCACAGTAATAATAATAAA 1364
         |||||||||||||| ||| |||||||||  |||||||||||||||||
Db 13959 ATGGGAGTGCGGCGGATGTAGGTC-CCAGTAAAAAATGCCTGAAATATACTCCGTCAAAC 13901

Qy  1365 AAAATAATGGTGATGGGTGTTCGTTCGGAAAGTTGGTAGAAAGATTCTGAAAATTCTTCATCTTCAG. 1424
         ||||| ||||||||||| |||||||||| ||||| ||||| ||||| ||||||||
Db 13900 ATATTAGGAAAGGCTTCGTTCGGAGTGGTCGGAAGTTGGTAGAAAGATACCTATGCAGGCGACATA 13841

Qy  1425 ATATTTTAAAGAAAAACATTATCAAGATTGAATTGAATTTAACTTACTGAAAATTCTTCTACCGTTA 1484
         ||||||| ||||||||||||||||||| ||||||   |||||||| |||||||||
Db 13840 ATGTCTTCATCTGGTATTAAT--ATTTCGGAGAGGCCACAATCAGATTCTTCTACCGTTA 13783

Qy  1485 AAGAAATTTATGAATTGAAGACTAAACAACCAACAACACCTTACAAATATGATGATCAATTAT 1544
         |||||||||||||||||||| |||||||||||  ||||| |||||||||||||||
Db 13782 CAGATGATTCTGCCTCCTAGGAGATACAACGAAAAGAATTTTGGAGACGATGATATTTCGA 13723

Qy  1545 CATTAACTTCATCTACACATCTTCTACTTCTCGATCTGGATCTGGGCAGTCGGCAGTGGAAATTGGTG 1604
         |||||||||||| |||||||||||||||||||||  ||||||||||||||||||||
Db 13722 CCGAAA-----------------------------ATGTTAAGTTTGGTG 13702

Qy  1605 GAGCAAGAATTTCTGATGGGATTAATGGAGGTTCATTACCTGTAATGAGAGTTTCACTTTTCC 1664
         |||||| |||||||||||||||||| |||||| |||||||
Db 13701 GTACAAGAATCAACGA-----TAATGATTCGGCATTGTCTGCCTGCTGAAAAGGTTTCCATTCTTTT 13648

Qy  1665 ANTTCTGAATCAGAAGAAACTATTCATGCCCCCGATATTCCTCGTGATATTCCTTCGTTGGTTAGAATTGGTGGAAACTTGGTGGTGGTTAGATTGTACTTGTC 1724
         |||| |||||| |||||||||||||||| ||||||||||||||||||||||||||||||
Db 13647 GTTCCGAATCAGAAGAAACAATACATGTCGTATTCCTGTATATTCCTGTGATGGTGGTTAGATTGGTGGCC 13588

Qy  1725 AATCTGTTCGAGATTTATTTAGAAATGGTGAAGAAACTTGGTGAAGAAATGTTGGCGCAAAGCATTTCATCCTTTAACTGCTG 1784
         |||||||||||| ||||||| |||||||||||||||||||| ||||| |||||||||||||||||||
Db 13587 AGAGTGTAAGCCGATTTGTTCAGAAATGTGAAGTGAAGAAATGTACATGGTGATTCATTTGGTATTCATTTGCC 13528

Qy  1785 CTACTGATTCGGAAGATCGGAAATGATCGGTGGCCAAAGCATTTGTGTATTCGTAAAGCATTTGGTCGTAAAGCATTTGGTCTAAAGCTG 1844
         |||||||| ||||| ||||| |||||||| |||||||||||||| |||||| |||||| |||||
Db 13527 CTACTGATGCGTGAAATGGTTGCGTAAAGCATTTGGTAAAGCATTTGGTCATTTGTGACAGCTG 13468

Qy  1845 AAGATATTCGAATGCAAGAAACTCGTGAAAAGTTGATTATTTAAAAGTTATTATTTTG 1904
         |||| ||||||||||| |||||||| ||||||||||||||||||
Db 13467 AAGATATTCGTATGCAAGAAACCCGTGAAAAGGTGAAAGTTGGAATTATTCAGAAACTATTATTTTG 13408

Qy  1905 TTTGTTTCCATACTTTTTGAAGGTGAATCAGAATTGTATAAATG 1964
         ||||||||||| ||||||| ||||||||||||
Db 13407 TTTGTTTCCATACTTTTGAAGGTGAATCAGGAATCAGAGACGATTACTTGGAGGCCGATTAACT 13348
```

```
Db  1619                                                           1678
         ||||||||||||||||||||||||||||||||||||||||||||||||||
         AAAAAGTTGAATTATTTAAAAAGTTATTATTTTGTTGTTCCATACTTTTGAAGCTGATA

Qy  1932 AAGAATCTGAAGATTAATTAGAACCGATAAAATGTTATATTGTGTTTCCATGATGGTA 1991
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1679 AAGAATCTGAAGATTAATTAGAACCGATAAAATGTTTATATTGTGTTTCCATGATGGTA 1738

Qy  1992 TATTAACGTTCCATTTTTCACCAATTTCTCATCCAGCAAATGTTAGAAGAAGAGTTCGTC 2051
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1739 TATTAACGTTCCATTTTTCACCAATTTCTCATCCAGCAAATGTTAGAAGAAGAGTTCGTC 1798

Qy  2052 AATTGAGAGATTATGTCGATGTGTAGTGCTGATTGGTTATGTTATGCCTTAATCGATGAAA 2111
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1799 AATTGAGAGATTATGTCGATGTGTAGTGGTTATGTTATGCCTTAATCGATGAAA 1858

Qy  2112 TTACCGATGGTTTTGCCCCCGTGATTCATGGAATTCATGATGAGCTGCATTGAAG 2171
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1859 TTACCGATGGTTTTGCCCCCGTGATTCATGGAATTGAATGTTGATGCCGCATTGAAG 1918

Qy  2172 ATGCCGTTTTCACTGCTAGAGATACTGATTTTAGTGTATGTTACAAAGAATTGGTGAAT 2231
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1919 ATGCCGTTTTCACTGCTAGAGATACTGATTTTAGTGTATGTTACAAAGAATTGGTGAAT 1978

Qy  2232 CAAGAAGAAAGTCATGACTTAATGAGATTATTATCAGTAAAGCTGATGTGTCATTAAAA 2291
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1979 CAAGAAGAAAGTCATGACTTAATGAGATTATTATCAGTAAAGCTGATGTGTCATTAAAA 2038

Qy  2292 TGTTTGCTAAAAGATGTCAAGAAGAAGCTAATTCTTCTTCGGTTATTATCAACGTCAAT 2351
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2039 TGTTTGCTAAAAGATGTCAAGAAGAAGCTAATTCTTCTTCGGTTATTATCAACGTCAAT 2098

Qy  2352 ATAACTTACAACAACAACAACA-----GGCCCCACCACCACCTAATCCTATTA 2405
         ||||||||||||||||||||     ||||||||||||||||||||
Db  2099 ATAACTTACAACAACAACAACAGGCCCCACCACCACCTAACCCTATTA 2158

Qy  2406 TTACTTCACCAATTAATCAACTTGAATCTTAATAGTTTAGGAGACTTCAACTCGGTGGAG 2465
         ||||||||||||||||||||||||  ||||||||||||||||||||||||
Db  2159 TTACTTCACCAATTAATCAACTTGAATCTTAATAGTTTAGGAGACTTCAACTCGGTGGAG 2218

Qy  2466 GAGTAGGAGTAGGAGGAGTGGAATTAATTTTGGTCCCAATCAACTTGGAAATAATAACTACTA 2525
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2219 GAGTACGAGTACGACGAATTAATTTTGGTCCCCATCCAACTTGGAAATAATAACTACTA 2278

Qy  2526 ATACTAATAACTACTGGTTCACCTTCACCACTTCAACAACAACAACAACACATGGTATCACTA 2585
         ||||||||||||||||||||||||||||||||||  |||||||||||||
Db  2279 ATACTAACACTACGGGTTCACCTTCACCACCTCACCACCT---CAACTACAAACACATGGTATCACTA 2335

Qy  2586 ACAAATCTTTCCCCATCCCC 2605
         ||||||||||||||||||||
Db  2336 ACAAATCTTTCCCCATCCCC 2355
```

RESULT 5
CR382138_14/c
WPCOMMENT   LOCUS CR382138 Accession CR382138
Sequence split into 24 fragments

Fragment Name	Begin	End
CR382138_00	1	110000
CR382138_01	100001	210000
CR382138_02	200001	310000
CR382138_03	300001	410000
CR382138_04	400001	510000
CR382138_05	500001	610000
CR382138_06	600001	710000
CR382138_07	700001	810000
CR382138_08	800001	910000
CR382138_09	900001	1010000
CR382138_10	1000001	1110000
CR382138_11	1100001	1210000
CR382138_12	1200001	1310000
CR382138_13	1300001	1410000
CR382138_14	1400001	1510000
CR382138_15	1500001	1610000

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 14:15:33 ; Search time 10845 Seconds
(without alignments)
12372.204 Million cell updates/sec

Title: US-10-018-105-3
Perfect score: 3525
Sequence: 1 tatataataataatatata.......tcaattattatcaatattgc 3525

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : BST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	359.8	10.2	912	9	CNS06I73	AL399925 T7 end of
c	2	301.6	8.6	1032	9	CNS0736W	AL427134 clone BA0
	3	211.2	6.0	1089	9	CNS06OJK	AL410742 T3 end of
c	4	210.8	6.0	798	9	CNS072G5	AL426171 clone BA0
c	5	202	5.7	579	8	BZ295013	BZ295013 CG1236.f1
	6	187.2	5.3	911	9	CNS06HIN	AL399045 T3 end of
	7	176	5.0	874	9	CNS06GW9	AL398239 T3 end of
	8	176	5.0	911	9	CNS06GN7	AL397913 T3 end of
	9	172.4	4.9	955	7	CO028936	CO028936 EST807320
	10	163	4.6	387	7	CO142543	CO142543 EST837214
	11	156.2	4.4	771	7	CF709049	CF709049 CCAGA79TR
	12	146	4.1	973	9	CNS06GSK	AL398106 T7 end of
	13	145.4	4.1	524	9	BZ297820	BZ297820 CG3653.r1
	14	143	4.1	763	1	AJ637812	AJ637812
	15	141.2	4.0	614	4	BM266292	BM266292 VL58 cDNA
	16	141	4.0	712	5	BQ743184	BQ743184 WHB4101_A
c	17	133.2	3.8	964	7	CO034119	CO034119 EST812503
	18	128.4	3.6	715	6	CD488599	CD488599 T11_F12 T
	19	122.6	3.5	850	9	CNS06K53	AL419293 T3 end of
	20	121.8	3.5	921	9	CNS075PZ	AL430413 clone BA0
	21	119.2	3.4	907	7	CO027928	CO027928 EST806312
	22	117	3.3	895	9	CNS06H1J	AL398429 T7 end of
c	23	114.8	3.3	934	7	CF823927	CF823927 EST701309
c	24	110.2	3.1	551	1	AJ637804	AJ637804 AJ637804
c	25	109.4	3.1	786	7	CF709038	CF709038 CCAGA79TF
c	26	108.6	3.1	1061	9	CNS07DEE	AL440364 T3 end of
c	27	108.2	3.1	901	7	CO011480	CO011480 EST799815
c	28	108	3.1	965	7	CF820256	CF820256 EST697638
c	29	106.6	3.0	641	8	AQ946120	AQ946120 Sheared D
	30	106	3.0	575	8	B2780846	B2780846 ii20h11.g
c	31	102.4	2.9	819	7	CF715298	CF715298 CCACQ57TF
	32	102.2	2.9	707	9	CG403581	CG403581 ZMMBBbO24
	33	100.6	2.9	815	7	CO025755	CO025755 EST804139
	34	100.6	2.9	823	7	CO025396	CO025396 EST803780
c	35	100.6	2.9	907	7	CO028288	CO028288 EST806672
c	36	100.6	2.9	932	7	CO025732	CO025732 EST804116
c	37	100.6	2.9	936	7	CO031086	CO031086 EST809470
c	38	100.6	2.8	989	7	CO028935	CO028935 EST807319
	39	100.4	2.8	413	5	BQ491813	BQ491813 EST00979
	40	99.8	2.8	587	8	BH873429	BH873429 hp45a07.b
c	41	99.8	2.8	781	8	BX145762	BX145762 Danio rer
	42	97.4	2.8	832	8	BH391984	BH391984 AG-ND-138
c	43	96.2	2.7	772	7	CF816703	CF816703 EST69408S
c	44	96	2.7	700	8	AQ940248	AQ940248 Sheared D
c	45	95.4	2.7	670	8	B2388480	B2388480 EINDL21TF

ALIGNMENTS

RESULT 1
CNS06I73/c
LOCUS   CNS06I73   912 bp   DNA   linear   GSS 30-NOV-2001
DEFINITION T7 end of clone AS0AA018C10 of library AS0A from strain CLIB 533
            of Saccharomyces bayanus, genomic survey sequence.
ACCESSION   AL399925
VERSION   AL399925.1 GI:1215087
KEYWORDS   GSS.
SOURCE   Saccharomyces bayanus
  ORGANISM Saccharomyces bayanus
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1 (bases 1 to 912)
  AUTHORS   Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
            Bolotin-Fukuhara,M., Bon,B., Brottier,P., Casaregola,S.,
            de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
            Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
            Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
            Wincker,P. and Weissenbach,J.
  TITLE   Genomic exploration of the hemiascomycetous yeasts: 1. A set of
            yeast species for molecular evolution studies
  JOURNAL   FEBS Lett. 487 (1), 3-12 (2000)
  MEDLINE   20584711
   PUBMED   11152876
REFERENCE   2 (bases 1 to 912)
  AUTHORS   Bon,B., Neuveglise,C., Casaregola,S., Artiguenave,F., Wincker,P.,
            Aigle,M. and Durrens,P.
  TITLE   Genomic exploration of the hemiascomycetous yeasts: 5.
            Saccharomyces bayanus var. uvarum
  JOURNAL   FEBS Lett. 487 (1), 37-41 (2000)
  MEDLINE   20584715
   PUBMED   11152880
REFERENCE   3 (bases 1 to 912)
  AUTHORS   Genoscope.
  TITLE   Direct Submission
  JOURNAL   Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
            2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
            segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT   This GSS is part of a random genomic sequencing program of thirteen
            yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
            exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
            Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
            lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
            angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
            Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
            5 kb were prepared and both extremities were sequenced. See
            keywords for description of this sequence and for the sequence of

```
                  GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:        April 14, 2005, 18:55:46 ; Search time 1925 Seconds
                                           (without alignments)
                                  11109.172 Million cell updates/sec

Title:         US-10-018-105-3
Perfect score: 3525
Sequence:      1 tatataatacatatatatata........tcaattattatcatcatattgc 3525

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      5622541 seqs, 303335566 residues

Total number of hits satisfying chosen parameters:    11245082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     Published Applications NA:*
          1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
          2: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
          3: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
          4: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
          5: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
          6: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
          7: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
          8: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
          9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
         10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
         11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
         12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
         13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
         14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
         15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
         16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
         17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
         18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
         19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
         20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
         21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
         22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	2769	78.6	2769	16	US-10-032-585-6675	Sequence 6675, Ap
2	179.6	5.1	1992	15	US-10-128-714-2563	Sequence 2563, Ap
3	179.6	5.1	1992	15	US-10-128-714-7563	Sequence 7563, Ap
4	118	3.3	462	11	US-09-864-408A-2265	Sequence 2265, Ap
5	117.6	3.3	8056	18	US-10-473-126-386	Sequence 386, App
6	116.4	3.3	688	18	US-10-653-047-7103	Sequence 7103, Ap
7	113.6	3.2	2048	15	US-10-128-714-1563	Sequence 1563, Ap
8	113.6	3.2	2048	15	US-10-128-714-6563	Sequence 6563, Ap
9	113.6	3.2	4048	15	US-10-128-714-563	Sequence 563, App
10	113.6	3.2	4048	15	US-10-128-714-5563	Sequence 5563, Ap
c 11	106.8	3.0	4985	14	US-10-094-240-10	Sequence 10, Appl
c 12	106.8	3.0	4985	16	US-10-056-405-10	Sequence 10, Appl
13	106.2	3.0	575	18	US-10-653-047-447	Sequence 447, App
14	97.4	2.8	286	18	US-10-425-115-137269	Sequence 137269,
15	94.4	2.7	969	18	US-10-363-345A-26081	Sequence 26081, A
16	94.4	2.7	969	18	US-10-363-345A-26082	Sequence 26082, A
c 17	94.4	2.7	969	19	US-10-363-483A-26081	Sequence 26081, A
18	94.4	2.6	8056	18	US-10-363-483A-26082	Sequence 26082, A
c 19	92.6	2.6	3996	14	US-10-473-126-386	Sequence 386, App
20	90	2.6	8056	18	US-10-087-464-42	Sequence 42, Appl
21	86.6	2.5	8056	18	US-10-473-126-240	Sequence 240, App
c 22	84.8	2.4	8056	18	US-10-473-126-240	Sequence 240, App
23	84	2.4	7676	15	US-10-240-485-151	Sequence 151, App
24	81.2	2.3	4985	14	US-10-094-240-10	Sequence 10, Appl
25	81.2	2.3	4985	15	US-10-056-405-10	Sequence 10, Appl
26	79.6	2.3	3931	15	US-10-006-780-1	Sequence 1, Appli
c 27	78.2	2.2	8759	18	US-10-473-126-104	Sequence 104, App
c 28	78.2	2.2	8759	18	US-10-473-126-232	Sequence 232, App
c 29	78.2	2.2	8759	18	US-10-473-126-250	Sequence 250, App
c 30	78.2	2.2	8759	18	US-10-473-126-378	Sequence 378, App
c 31	77.4	2.2	535	18	US-10-363-345A-28883	Sequence 28883, A
32	77.4	2.2	535	18	US-10-363-345A-28884	Sequence 28884, A
33	77.4	2.2	535	19	US-10-363-483A-28883	Sequence 28883, A
c 34	77	2.2	535	19	US-10-363-483A-28884	Sequence 28884, A
35	76.2	2.2	5163	15	US-10-311-455-1221	Sequence 1221, Ap
c 36	75.4	2.2	564	18	US-10-437-963-7175	Sequence 7175, Ap
c 37	74.8	2.1	17183	15	US-10-311-455-460	Sequence 460, App
c 38	74.6	2.1	16766	15	US-10-311-455-2130	Sequence 2130, Ap
39	74.4	2.1	19380	17	US-10-221-613-389	Sequence 389, App
40	74.4	2.1	7025	17	US-10-257-166-142	Sequence 142, App
c 41	74.4	2.1	7025	17	US-10-240-454-46	Sequence 46, Appl
c 42	74.4	2.1	50000	19	US-10-706-635-23	Sequence 23, Appl
43	74	2.1	83391	18	US-10-433-793-123	Sequence 123, App
44	73.4	2.1	642	16	US-10-032-585-6714	Sequence 6714, Ap
45	73.4	2.1	34688	18	US-10-433-793-89	Sequence 89, Appl

ALIGNMENTS

```
RESULT 1
US-10-032-585-6675
; Sequence 6675, Application US/10032585
; Publication No. US2003018095A1
; GENERAL INFORMATION:
;  APPLICANT: Terry, Roemer D.
;  APPLICANT: Bo, Jiang
;  APPLICANT: Charles, Boone
;  APPLICANT: Howard, Bussey
;  TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
;  FILE REFERENCE: 10182-005-999
;  CURRENT APPLICATION NUMBER: US/10/032,585
;  CURRENT FILING DATE: 2001-12-20
;  SOFTWARE: Patentin version 3.1
;  NUMBER OF SEQ ID NOS: 8000
;  SEQ ID NO 6675
;  LENGTH: 2769
;  TYPE: DNA
;  ORGANISM: Candida albicans
US-10-032-585-6675

Query Match       78.6%;   Score 2769;   DB 16;   Length 2769;
Best Local Similarity  100.0%;   Pred. No. 0;
Matches 2769;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   338 ATGTCCGATAGTGAAAGTTATTATCAAAATTCAACTACTAATCAACCTATTCCTAGATCT 397
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGTCCGATAGTGAAAGTTATTATCAAAATTCAACTACTAATCAACCTATTCCTAGATCT 60

Qy   398 GATGAAGTATTGGATGATGATCATAGAAATCAAAATCACTAAATGATTGTGCCATTAGTGATAGT 457
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GATGAAGTATTGGATGATGATCATAGAAATCAAAATCACTAAATGATTGTGCCATTAGTGATAGT 120

Qy   458 GAAGATGAGTTGGGAATTAAAATCAGAATTAAAATCAGAAGTTGTAAAAGCGAAAAACAA 517
```

```
Db   121 GAAGATGAGTTGGAATCAGAATTAGAAATCAGAATTAGAAGATACATCAGAATTAGAAT  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   518 CAACACATCATCAGAGATTACATCAGAGATAATGCTAAACCATTGACTCGTAAATCTGGT  577

Db   181 CAACACATCATCAGAGATTACATCAGAGATAATGCTAAACCATTGACTCGTAAATCTGGT  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   578 TCTTCAATTAAGAAAAAATCTAATCTTACCGATAAAGATAGAATTACCAACCCTATGAGT  637

Db   241 TCTTCAATTAAGAAAAAATCTAATCTTACCGATAAAGATAGAATTACCAACCCTATGAGT  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   638 TTAATCTGGTGGTGATGATCTATTAACACGGTCACAAAAATCGTAATTATACACATGAT  697

Db   301 TTAATCTGGTGGTGATGATCTATTAACACGGTCACAAAAATCGTAATTATACACATGAT  360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   698 TCATTACGTAAAGATTTTATTTAAAGATAATACTGACGACAATTCTACTAATAATCAT  757

Db   361 TCATTACGTAAAGATTTTATTTAAAGATAATACTGACGACAATTCTACTAATAATCAT  420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   758 ACTCATCTGCAATTCCAATTCCAATTCCAACCCAATTATTACTAATGCTAAT  817

Db   421 ACTCATCTGCAATTCCAATTCCAATTCCAACCCAATTATTACTAATGCTAAT  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   818 AAATCAAGAAGAAATCTCAATTGGAAAATTTACCTCCATTAATTAAAAGAAAACATT  877

Db   481 AAATCAAGAAGAAATCTCAATTGGAAAATTTACCTCCATTAATTAAAAGAAAACATT  540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   878 GGTCGTAATAATTCTAATAATTTGAAAATGATTTAGTTAGTCCCATGACAAAAATGAAA  937

Db   541 GGTCGTAATAATTCTAATAATTTGAAAATGATTTAGTTAGTCCCATGACAAAAATGAAA  600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   938 ACTAATGATAGTGAAGATATTACTAATACTAGCACCACTGCTAATCATCATATGAACTGGT  997

Db   601 ACTAATGATAGTGAAGATATTACTAATACTAGCACCACTGCTAATCATCATATGAACTTGGT  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   998 ATTGGTGCTACAACCCTTGGTGTTGGAACTGGTACACCGCCACTGCCACTGCCACTGCT 1057

Db   661 ATTGGTGCTACAACCCTTGGTGTTGGAACTGGTACACCGCCACTGCCACTGCCACTGCT  720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1058 GCTGCTGGTAGAGACCATCTCGTTCATCTATTGATAGTGAAGCTGAAGTTCTCATGCATCA 1117

Db   721 GCTGCTGGTAGAGACCATCTCGTTCATCTATTGATAGTGAAGCTGAAGTTCTCATGCATCA  780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1118 AGATCATCTCAAGAGAACTCGAAGAAGATGGTTGTTTTCCTATGGTTGTTTTCCTATGGTTGGTGATCATATTAGA 1177

Db   781 AGATCATCTCAAGAGAACTCGAAGAAGATGGTTGTTTTCCTATGGTTGGTGATCATATTAGA  840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1178 GTTTAATGGAATTGATTTGATGAATTTATTAGAGAAGAAGAGAGAAGAGCT 1237

Db   841 GTTTAATGGAATTGATTTGATGAATTTATTAGAGAAGAAGAGAGAAGAGCT  900
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1238 TATTTACAAAAACAAAATGATTGCTAAAAATATTCTGCGTAATTGAATTTGATGAATTTCAAAATCTT 1297

Db   901 TATTTACAAAAACAAAATGATTGCTAAAAATATTCTGCGTAATTGAATTTGATGAATTTCAAAATCTT  960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1298 TCCAAAAATAATAATACTACTAGGTGGTCGTGCCATCTCGTCATCCATATCAGATAATAAT 1357

Db   961 TCCAAAAATAATAATACTACTAGGTGGTCGTGCCATCTCGTCATCCATATCAGATAATAAT 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1358 AATAAAAAAAATAATGGTGGTGATGCGTGATGGGTGGTTCAGTATGGCAGCATTAAAATATACT 1417

Db  1021 AATAAAAAAAATAATGGTGGTGATGCGTGATGGGTGGTTCAGTATGGCAGCATTAAAATATACT 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1418 CCAAAAATATTTTAAAGAAAAACATTTCAAGATTTGAATTTACTCATGCTTACTCATGATGAT 1477

Db  1081 CCAAAAATATTTTAAAGAAAAACATTTCAAGATTTGAATTTACTCATGAATTTACTCATGATGAT 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1478 TCTTCAGAAGAAATTTATGGAAGACTAAGACTAAACAACAACCACCTTACAAATATGATGAT 1537

Db  1141 TCTTCAGAAGAAATTTATGATGAATTGAAGACTAAACAACAACCACCTTACAAATATGATGAT 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1538 CAATTATCATTAACTTCATCTACACATCTTCTACTTCTGCGATCTGGGATCTGGGCAGGTGAAA 1597
```

```
Db  1201 CAATTATCATTAACTTCATCTACACATCTTCTACTTCTGCGATCTGGGATCTGGGCAGGTGAAA 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1598 TTTGGTGGAGCAAGAATTCTGATGGGATTAATGGATCTTCATTACCTGATGATTTTCA 1657

Db  1261 TTTGGTGGAGCAAGAATTCTGATGGGATTAATGGATCTTCATTACCTGATGATTTTCA 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1658 CTTTTCCATTCTGAATCAGAAGAAACTCATGCCCCCGATATTCCATCATTAGTATCA 1717

Db  1321 CTTTTCCATTCTGAATCAGAAGAAACTCATGCCCCCGATATTCCATCATTAGTATCA 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1718 CCAGGTCAATCTGTTCGTGAGATTTATTTAGAAAATGGTGAAGAAACTTCGTGGTTAGATTGT 1777

Db  1381 CCAGGTCAATCTGTTCGTGAGATTTATTTAGAAAATGGTGAAGAAACTTCGTGGTTAGATTGT 1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1778 ACTTGTCCTACTGATTCGGATTCGGATGGTTGGCCAAAGCATTTGGTATTCATCCTTTA 1837

Db  1441 ACTTGTCCTACTGATTCGGATTCGGATGGTTGGCCAAAGCATTTGGTATTATTCCTTTA 1500
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1838 ACTGCTGAAGATATTCGAAGAACTCGTGAAAAAAGTTGAATTATTTAAAAGTTAT 1897

Db  1501 ACTGCTGAAGATATTCGAAGAACTCGTGAAAAAAGTTGAATTATTTAAAAGTTAT 1560
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1898 TATTTGTTGTTTCCATACTTTTGAAGCTGATAAAGAATCTGAAGATTATTTAGAACCG 1957

Db  1561 TATTTGTTGTTTCCATACTTTTGAAGCTGATAAAGAATCTGAAGATTATTTAGAACCG 1620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1958 ATAAATGTTATATGTTGTTTCCATGATGGTATATAACGTTCCATTTTCACCAATT 2017

Db  1621 ATAAATGTTATATGTTGTTTCCATGATGGTATATAACGTTCCATTTTCACCAATT 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2018 TCTCATCCAGCAAATGTTAGAGAAGAGTTCGTCAATTGAGAGTATGTCGATGTTAGT 2077

Db  1681 TCTCATCCAGCAAATGTTAGAGAAGAGTTCGTCAATTGAGAGTATGTCGATGTTAGT 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2078 GCTGATTGGTTATGTTATGTCCTTAATCGATGAAATTACCGATGTTTGCCCCGTGATT 2137

Db  1741 GCTGATTGGTTATGTTATGTCCTTAATCGATGAAATTACCGATGTTTGCCCCGTGATT 1800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2138 CATGGAATTGAATAGAAGCTGATGCCATTGAAGATGCCGTTTTCACTGCTGCTAGAGATACT 2197

Db  1801 CATGGAATTGAATAGAAGCTGATGCCATTGAAGATGCCGTTTTCACTGCTGCTAGAGATACT 1860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2198 GATTTTAGTAGTATGTTACAAAGAATTGGTGAATCAAGAGAAAAGTCATGAGACTTTAATG 2257

Db  1861 GATTTTAGTAGTATGTTACAAAGAATTGGTGAATCAAGAGAAAAGTCATGAGACTTTAATG 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2258 AGAATTATTATCAGGTAAAGCTGTAAAAGATGTCAAAAAAGATGTCAAGAGAGAA 2317

Db  1921 AGAATTATTATCAGGTAAAGCTGTAAAAGATGTCAAAAAAGATGTCAAGAGAGAA 1980
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2318 GCTAATTCTTCTTCGTTATTATCCAATATCAATATAACTTACACAACAACAACAACAG 2377

Db  1981 GCTAATTCTTCTTCGTTATTATCCAATATCAATATAACTTACACAACAACAACAACAG 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2378 GCCCCACCACCACCACCACCACCACCTAGTAATCCTATTATTACTTCAACTTTGAATCTT 2437

Db  2041 GCCCCACCACCACCACCACCACCACCTAGTAATCCTATTATTACTTCAACTTTGAATCTT 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2438 AATAGTTTAGGAACTTCAACTGGTGGAGGAGTTAGGAGGAATTAATTTTGGTCCC 2497

Db  2101 AATAGTTTAGGAACTTCAACTGGTGGAGGAGTTAGGAGGAATTAATTTTGGTCCC 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2498 AATCCAACTGGAAATATAACATGGTATCACAACAACAATCTTCCCCATCCGGTTCACCACCT 2557

Db  2161 AATCCAACTGGAAATATAACATGGTATCACAACAACAATCTTCCCCATCCGGTTCACCACCT 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2558 CAACAACAACAACAACATGGTATCACAACAACAATCTTCCCCATCCCGATGCCACGTCCA 2617

Db  2221 CAACAACAACAACAACATGGTATCACAACAACAATCTTCCCCATCCCGATGCCACGTCCA 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2618 AGAGCTGATATTGCATTATTAGGTGATATTCAAGATCATAATAATCACCATGTTTCAA 2677

Db  2281 AGAGCTGATATTGCATTATTAGGTGATATTCAAGATCATAATAATCACCATGTTTCAA 2340
```

Qy   2678 AATTTATTAGCCTATGAAAAAATTTTCAGTCGTTCACATTCAAATTATTTAGCTCAATTA 2737
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATTTATTAGCCTATGAAAAAATTTTCAGTCGTTCACATTCAAATTATTTAGCTCAATTA 2400

Qy   2738 CAAGTTGAATCATTCATTCAATTCCAATAATAAAATCACCGAAATGTTTTCTAAAATTACTTTG 2797
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   2401 CAAGTTGAATCATTCATTCAATTCCAATAATAAAATCACCGAAATGTTTTCTAAAATTACTTTG 2460

Qy   2798 ATTGGGACAAATGTTAGTTCCATTAAATTAGTCACGGGACTTTTTGTATGAATGTAAGA 2857
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 ATTGGGACAAATGTTAGTTCCATTAAATTAGTCACGGGACTTTTTGTATGAATGTAAGA 2520

Qy   2858 GTCCCTGGTGAAGGTGTACCCAATTTAGGTTGGTTTTTCGGAATTGTTGGAGTATTAATA 2917
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 GTCCCTGGTGAAGGTGTACCCAATTTAGGTTGGTTTTTCGGAATTGTTGGAGTATTAATA 2580

Qy   2918 TTTATATAATTATTGGATCATTATATTGCTCAATGTGGTGAAAAAAATTGAATAATTCA 2977
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTTATATAATTATTGGATCATTATATTGCTCAATGTGGTGAAAAAAATTGAATAATTCA 2640

Qy   2978 ATTGAAGGACAAAATAATGGTAATCGACCAATTTTAATCATTCATCAAGAAGATCAATT 3037
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 ATTGAAGGACAAAATAATGGTAATCGACCAATTTTAATCATTCATCAAGAAGATCAATT 2700

Qy   3038 AGAAGTTTAGGTTTAAAAAAACATGGTGGTAATAAAATCAATTATTAGTTTCCCCAATAAA 3097
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 AGAAGTTTAGGTTTAAAAAAACATGGTGGTAATAAAATCAATTATTAGTTTCCCCAATAAA 2760

Qy   3098 TATGAATAA 3106
            |||||||||
Db   2761 TATGAATAA 2769

RESULT 2
US-10-128-714-2563
; Sequence 2563, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wenqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2563
; LENGTH: 1992
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-2563

Query Match   5.1%; Score 179.6; DB 15; Length 1992;
Best Local Similarity 56.6%; Pred. No. 3e-20;
Matches   376; Conservative   0; Mismatches 279; Indels   9; Gaps   2;

Qy   1659 TTTTCCATTCTGAATCAGAAGAAGAACTATTCATCCCCCCGATATTCCATCATTAGTATCAC 1718

Db   959 TTTTCTCATCCGAGTCCCAGAGCACTGTGCATGCGGCGGGGAACTGGGGCACCTGTCGTGCTCC 1018
             ||||| || |||||| |||||||||||||||||| ||||||||||||||||
Qy   1719 CAGGTCAATCGTTCGAGATTTATTTAGAAATGG------TGAAGAAACTTGGTGGTTAG 1772
             |||||||||||||||||||||||||||||||| ||||| |||||||||||
Db   1019 CTGGTGATACTTTCCGGGATCTCTTTCAACTTGGCCCGGAGGAGGTGTGTGGTGGTTGG 1078

Qy   1773 ATTGTACTTGTCCTACTGATTCGGAAATGAAAATGTTGGCCAAAGCATTTGGTATTCATC 1832
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1079 ACGTACTCAACAAGAGGAGAAGTTGCTGCACTCTCGCGGGCATTTCCATCCATC 1138

Qy   1833 CTTTAACTGCTGAAGATATTCGAATGCAAGAAACTCTGTGAAAAAGTTGAATTATTAAAA 1892
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1139 CACTGACTACCGAAGATATCTTGACTCAAGAAGCCCGTGAAAAGGTCGAGCTTTTCAAGC 1198

Qy   1893 GTTATTATTTTGTTGTTCCATACTTT---TGAAGCTGATAAAGAATCTGAAGATTATT 1949
             ||||||||||||||||||||||||| |||||||||| ||||||||||||||||
Db   1199 AATATTACTTTGTCTCGCTTCCGGACATTCTATCAGCTCGACAACAGAGAACGACGCCTCA 1258

Qy   1950 TAGAACCGATAAAATGTTTATATTGTTGTTTTCCGGACGTGTCCTCTCATTCTCATTCA 2009
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1259 TGGAGCCCGTCAACTTCACATGGTTGTTTTCCGGACGGTGGTCAATTGAGAGATTATGTCG 1318

Qy   2010 CACCAATTTCTCATCCAGCAAATGTTAGAAGAAGTTCGTCAATTGAGAGATTATGTCG 2069
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1319 CCGAGAATCCACACGCGGCAAATGTCAGGAAGAAGAATTGGGAAGCTTCGTGATTTATGTGT 1378

Qy   2070 ATGTTAGTGCTGATTGGTTATGTTATGCCTTAATCGATGAAAATTACCGATGGTTTGCCC 2129
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1379 CCCTCAGTAGTGACTGGAATCGTGTTATGCCATGAATGAAGATGCCGTTTTCACTCGTA 1438

Qy   2130 CCGTGATTCATGGAATTGAAATGATGAAGCTGAATCAAGAAGAAAAGTCATGA 2189
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1439 CTGTCATCCGACGAGATTGAGATGATCGAATCGAGCCAATTGAGGACCTCGTTTTCATCGCGC 1498

Qy   2190 GAGATACTGATTTTAGTAGTATGTTACAAAGAAGAATTGGTGAATCAAGAGAGAAAAGTCATGA 2249
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1499 GCGTCGACGATTTTGAATCCTTCTTACCCGGAATCGGTGGCCTTCGTAAGAGGTCATGA 1558

Qy   2250 CTTTAATGAGATTATTATTCAGGTAAAGCTGATGTCATTAAAATGTTTGCTAAAAGATGTC 2309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1559 GCTTGATGCGCCTTCTAGGTGGCAAAGCAGATGTCATTCATTCGCGGTTTCTCCAAGCGTTGCA 1618

Qy   2310 AAGA 2313
             ||||
Db   1619 ACGA 1622

RESULT 3
US-10-128-714-7563
; Sequence 7563, Application US/10128714
; Publication No. US2003011901301A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wenqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362